Figure 1 Sequences of antibodies specific for TGFbeta1

(a) Antibodies to TGFbeta1 isolated directly from repertoires

(i) 1B2 VH (also known as 7A3 VH)

Sequence Range: 1 to 369

```
          10          20          30          40
     *    *    *      *    *      *    *      *    *
CAG GTG CAA CTG GTG GAG TCT GGG GGA GGC GTG GTC CAG CCT GGG AGG
 Q   V   Q   L   V   E   S   G   G   G   V   V   Q   P   G   R>
___a___a___a____TRANSLATION OF 7A3 VH.SEQ [A]__a___a___a___a___>

50          60          70          80          90
 *     *    *     *     *     *     *     *     *     *
TCC CTG AGA CTC TCC TGT GCA GCC TCT GGA TTC ACC TTC AGT AGC TAT
 S   L   R   L   S   C   A   A   S   G   F   T   F   S   S   Y>
___a___a___a____TRANSLATION OF 7A3 VH.SEQ [A]__a___a___a___a___>

  100         110         120         130         140
    *    *      *     *     *     *     *     *     *
GGC ATG CAC TGG GTC CGC CAG GCT CCA GGC AAG GGG CTG GAG TGG GTG
 G   M   H   W   V   R   Q   A   P   G   K   G   L   E   W   V>
___a___a___a____TRANSLATION OF 7A3 VH.SEQ [A]__a___a___a___a___>

    150         160         170         180         190
*     *     *     *     *     *     *     *     *     *
GCA GTT ATA TCA TAT GAT GGA AGT AAT AAA TAC TAT GCA GAC TCC GTG
 A   V   I   S   Y   D   G   S   N   K   Y   Y   A   D   S   V>
___a___a___a____TRANSLATION OF 7A3 VH.SEQ [A]__a___a___a___a___>

       200         210         220         230         240
  *     *     *     *     *     *     *     *     *     *
AAG GGC CGA TTC ACC ATC TCC AGA GAC AAT TCC AAG AAC ACG CTG TAT
 K   G   R   F   T   I   S   R   D   N   S   K   N   T   L   Y>
___a___a___a____TRANSLATION OF 7A3 VH.SEQ [A]__a___a___a___a___>
```

```
                250         260         270         280
      *       *       *       *       *       *       *       *
CTG CAA ATG AAC AGC CTG AGA GCT GAG GAC ACG GCT GTG TAT TAC TGT
 L   Q   M   N   S   L   R   A   E   D   T   A   V   Y   Y   C>
___a___a___a____TRANSLATION OF 7A3 VH.SEQ [A]__a___a___a___a___>

290         300         310         320         330
 *       *       *       *       *       *       *       *       *
GCG AAA ACT GGG GAA TAT AGT GGC TAC GAT TCT AGT GGT GTG GAC GTC
 A   K   T   G   E   Y   S   G   Y   D   S   S   G   V   D   V>
___a___a___a____TRANSLATION OF 7A3 VH.SEQ [A]__a___a___a___a___>

  340         350         360
    *       *       *       *       *       *
TGG GGC AAA GGG ACC ACG GTC ACC GTC TCC TCA (SEQ ID NO:7)
 W   G   K   G   T   T   V   T   V   S   S> (SEQ ID NO:8)
___a__TRANSLATION OF 7A3 VH.SEQ [A]_____a___>
```

(ii) 1A-E5 VH

Sequence Range: 1 to 345

```
            10          20          30          40
      *       *       *       *       *       *       *       *
GAG GTG CAG CTG GTG GAG TCT GGT GGA GGC TTA GTT CAG CCT GGG GGG
 E   V   Q   L   V   E   S   G   G   G   L   V   Q   P   G   G>
___a___a___a___a_TRANSLATION OF 1AE-5 VH [A]___a___a___a___a___>

50          60          70          80          90
 *       *       *       *       *       *       *       *       *
TCC CTG AGA CTC TCC TGT GCA GCC TCT GGA TTC ACC TTC AGT AGC TAC
 S   L   R   L   S   C   A   A   S   G   F   T   F   S   S   Y>
___a___a___a___a_TRANSLATION OF 1AE-5 VH [A]___a___a___a___a___>

  100         110         120         130         140
    *       *       *       *       *       *       *       *
```

```
TGG ATG CAC TGG GTC CGC CAA GCT CCA GGG AAG GGG CTG GTG TGG GTC
 W   M   H   W   V   R   Q   A   P   G   K   G   L   V   W   V>
___a___a___a___a_TRANSLATION OF 1AE-5 VH [A]___a___a___a___a___>

    150           160           170           180           190
*     *       *       *     *       *     *     *       *     *
TCA CGT ATT AAT AGT GAT GGG AGT AGC ACA AGC TAC GCG GAC TCC GTG
 S   R   I   N   S   D   G   S   S   T   S   Y   A   D   S   V>
___a___a___a___a_TRANSLATION OF 1AE-5 VH [A]___a___a___a___a___>

        200           210           220           230           240
  *       *       *     *       *       *     *       *       *
AAG GGC CGA TTC ACC ATC TCC AGA GAC AAC GCC AAG AAC ACG CTG TAT
 K   G   R   F   T   I   S   R   D   N   A   K   N   T   L   Y>
___a___a___a___a_TRANSLATION OF 1AE-5 VH [A]___a___a___a___a___>

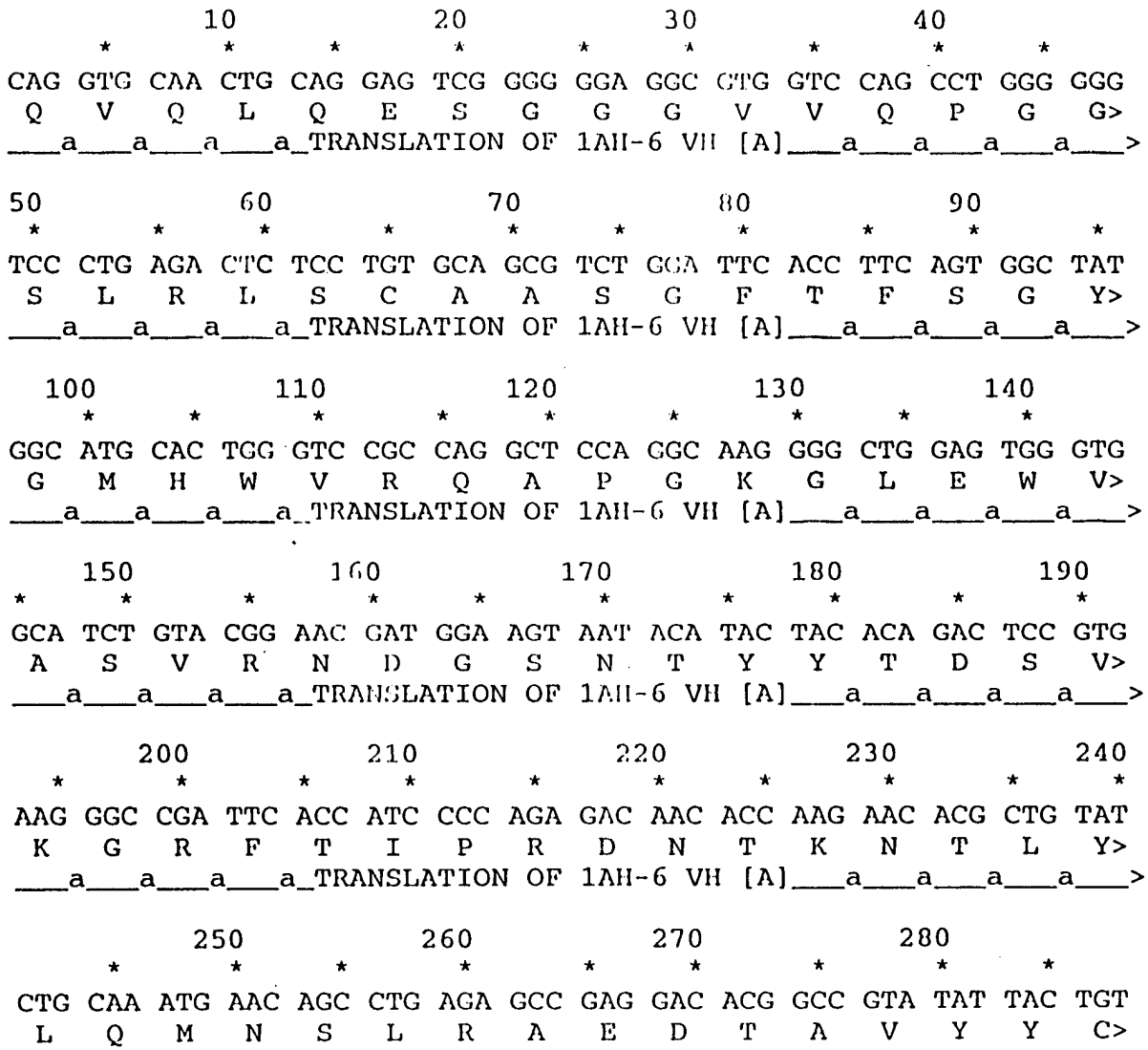
            250           260           270           280
      *       *     *       *       *     *       *       *
CTG CAA ATG AAC AGT CTG AGA GCC GAG GAC ACG GCC GTG TAT TAC TGT
 L   Q   M   N   S   L   R   A   E   D   T   A   V   Y   Y   C>
___a___a___a___a_TRANSLATION OF 1AE-5 VH [A]___a___a___a___a___>

290           300           310           320           330
  *       *       *       *       *     *       *       *
GCA AGG GAG AAT AGT TAT GTG CCT TGG GGG CAG GGC ACC CTG GTC ACC
 A   R   E   N   S   Y   V   P   W   G   Q   G   T   L   V   T>
___a___a___a___a_TRANSLATION OF 1AE-5 VH [A]___a___a___a___a___>

  340
    *     *
GTC TCC TCA (SEQ ID NO:113)
 V   S   S> (SEQ ID NO:111)
___a___a___>
```

(iii) 1A-H6 VH

Sequence Range: 1 to 354



```
___a___a___a___a_TRANSLATION OF 1AH-6 VH [A]___a___a___a___a___>

290           300           310           320           330
 *       *     *       *     *       *     *       *     *       *
ACG TCT GAT CCT TTA CGC TAT CCT ATT GAC TAC TGG GGC CAG GGA ACC
 T   S   D   P   L   R   Y   P   I   D   Y   W   G   Q   G   T>
___a___a___a___a_TRANSLATION OF 1AH-6 VH [A]___a___a___a___a___>

  340           350
    *       *     *
CTG GTC ACC GTC TCG AGT (SEQ ID NO: 114)
 L   V   T   V   S   S> (SEQ ID NO: 112)
___TRANSLATION OF 1____>
```

(iv) 31G9 VH

Sequence Range: 1 to 369

```
            10            20            30            40
     *       *     *       *     *       *     *       *     *
CAG GTG CAG CTG GTG CAG TCT GGG GGA GGC GTG GTC CAG CCT GGG AGG
 Q   V   Q   L   V   Q   S   G   G   G   V   V   Q   P   G   R>
___a___a___a____TRANSLATION OF 31G9 VH.SEQ [A]_a___a___a___a___>

50            60            70            80            90
 *       *     *       *     *       *     *       *     *       *
TCC CTG AGA CTC TCC TGT GCA GCC TCT GGA TTC ACC TTC AGT AGC TAT
 S   L   R   L   S   C   A   A   S   G   F   T   F   S   S   Y>
___a___a___a____TRANSLATION OF 31G9 VH.SEQ [A]_a___a___a___a___>

  100           110           120           130           140
    *       *     *       *     *       *     *       *     *
GGC ATG CAC TGG GTC CGC CAG GCT CCA GGC AAG GGG CTG GAG TGG GTG
 G   M   H   W   V   R   Q   A   P   G   K   G   L   E   W   V>
___a___a___a____TRANSLATION OF 31G9 VH.SEQ [A]_a___a___a___a___>
```

```
    150          160          170          180          190
*    *    *    *    *    *    *    *    *    *
GCA GTT ATA TCA TAT GAT GGA AGT ATT AAA TAC TAT GCA GAC TCC GTG
 A   V   I   S   Y   D   G   S   I   K   Y   Y   A   D   S   V>
___a___a___a____TRANSLATION OF 31G9 VH.SEQ [A]_a___a___a___a___>

       200          210          220          230          240
  *    *    *    *    *    *    *    *    *    *
AAG GGC CGA TTC ACC ATC TCC AGA GAC AAT TCC AAG AAC ACG CTG TAT
 K   G   R   F   T   I   S   R   D   N   S   K   N   T   L   Y>
___a___a___a____TRANSLATION OF 31G9 VH.SEQ [A]_a___a___a___a___>

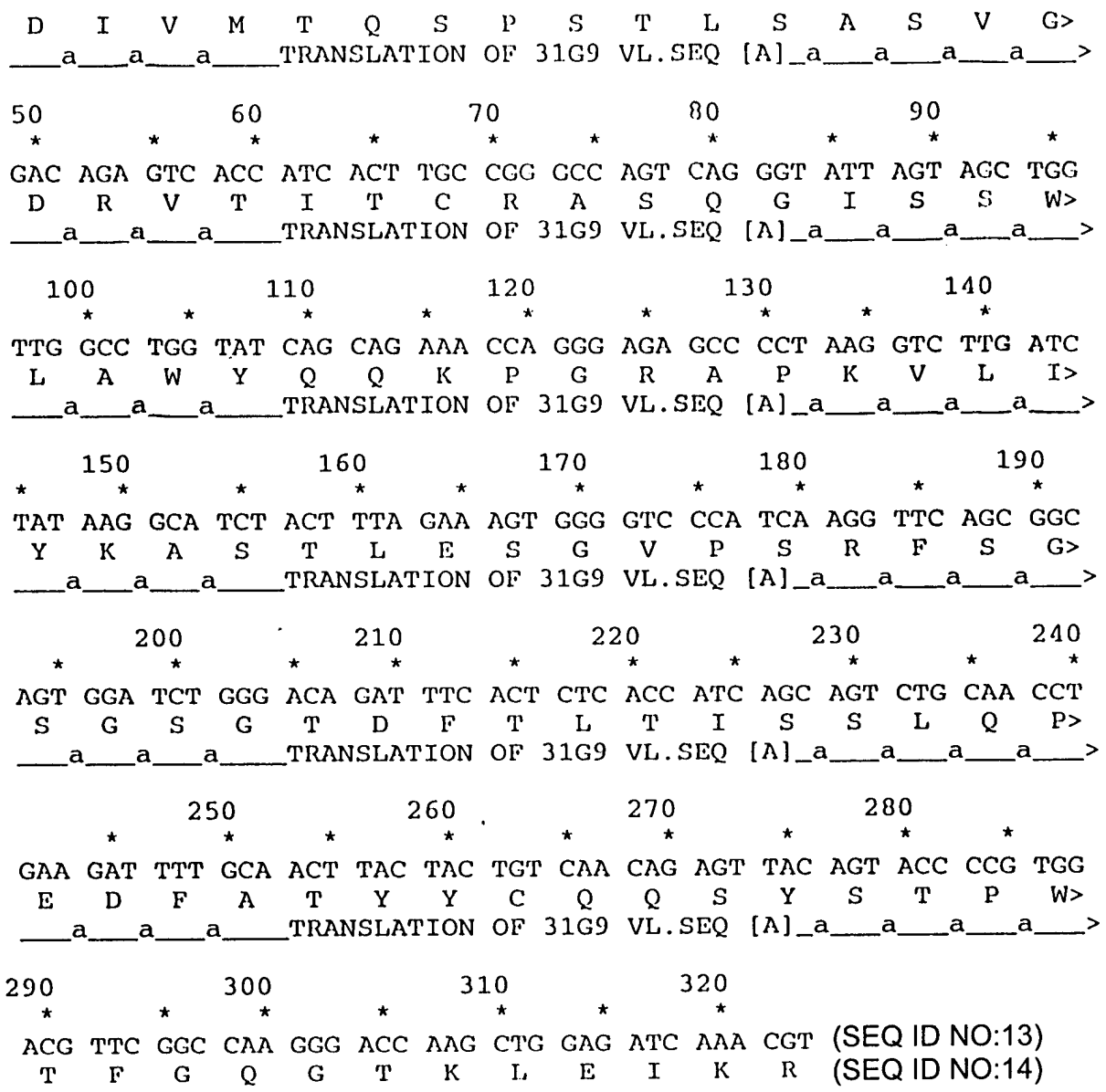
          250          260          270          280
     *    *    *    *    *    *    *    *    *
CTG CAA ATG AAC AGC CTG AGA GCT GAG GAC ACG GCT GTG TAT TAC TGT
 L   Q   M   N   S   L   R   A   E   D   T   A   V   Y   Y   C>
___a___a___a____TRANSLATION OF 31G9 VH.SEQ [A]_a___a___a___a___>

290          300          310          320          330
  *    *    *    *    *    *    *    *    *    *
GCG CGA ACT GGT GAA TAT AGT GGC TAC GAT ACG AGT GGT GTG GAG CTC
 A   R   T   G   E   Y   S   G   Y   D   T   S   G   V   E   L>
___a___a___a____TRANSLATION OF 31G9 VH.SEQ [A]_a___a___a___a___>

  340          350          360
    *    *    *    *    *    *
TGG GGG CAA GGG ACC ACG GTC ACC GTC TCC TCA (SEQ ID NO:9)
 W   G   Q   G   T   T   V   T   V   S   S> (SEQ ID NO:10)
___a__TRANSLATION OF 31G9 VH.SEQ [A]
```

(v) 31G9 VL

```
          10           20           30           40
     *    *    *    *    *    *    *    *    *
GAC ATC GTG ATG ACC CAG TCT CCT TCC ACC CTG TCT GCA TCT GTA GGA
```


D I V M T Q S P S T L S A S V G>
___a___a___a____TRANSLATION OF 31G9 VL.SEQ [A]_a___a___a___a___>
50 60 70 80 90
GAC AGA GTC ACC ATC ACT TGC CGG GCC AGT CAG GGT ATT AGT AGC TGG
D R V T I T C R A S Q G I S S W>
___a___a___a____TRANSLATION OF 31G9 VL.SEQ [A]_a___a___a___a___>
100 110 120 130 140
TTG GCC TGG TAT CAG CAG AAA CCA GGG AGA GCC CCT AAG GTC TTG ATC
L A W Y Q Q K P G R A P K V L I>
___a___a___a____TRANSLATION OF 31G9 VL.SEQ [A]_a___a___a___a___>
150 160 170 180 190
TAT AAG GCA TCT ACT TTA GAA AGT GGG GTC CCA TCA AGG TTC AGC GGC
Y K A S T L E S G V P S R F S G>
___a___a___a____TRANSLATION OF 31G9 VL.SEQ [A]_a___a___a___a___>
200 210 220 230 240
AGT GGA TCT GGG ACA GAT TTC ACT CTC ACC ATC AGC AGT CTG CAA CCT
S G S G T D F T L T I S S L Q P>
___a___a___a____TRANSLATION OF 31G9 VL.SEQ [A]_a___a___a___a___>
250 260 270 280
GAA GAT TTT GCA ACT TAC TAC TGT CAA CAG AGT TAC AGT ACC CCG TGG
E D F A T Y Y C Q Q S Y S T P W>
___a___a___a____TRANSLATION OF 31G9 VL.SEQ [A]_a___a___a___a___>
290 300 310 320
ACG TTC GGC CAA GGG ACC AAG CTG GAG ATC AAA CGT (SEQ ID NO:13)
T F G Q G T K L E I K R (SEQ ID NO:14)

___a___a___a____TRANSLATION OF 31G9 VL.SEQ [A]_

Figure 1 (b) Light chains of antibodies to TGFbeta1 isolated by chain shuffling

FIG. 1(b) (i) 7A3 VL

Sequence Range: 1 to 342

```
          10          20          30          40
     *    *    *      *    *      *    *      *    *
GAC ATC GTG ATG ACC CAG TCT CCA GAC TCC CTG GCT GTG TCT CTG GGC
 D   I   V   M   T   Q   S   P   D   S   L   A   V   S   L   G>
___a___a___a____TRANSLATION OF 7A3 VL.SEQ [A]__a___a___a___a___>

50          60          70          80          90
 *     *    *     *     *     *     *     *     *     *
GAG AGG GCC ACC ATC AAC TGC AAG TCC AGC CAG AGT CTT TTA TAC AGC
 E   R   A   T   I   N   C   K   S   S   Q   S   L   L   Y   S>
___a___a___a____TRANSLATION OF 7A3 VL.SEQ [A]__a___a___a___a___>

  100         110         120         130         140
    *     *     *     *     *     *     *     *     *
TAC AAC AAG ATG AAC TAC TTA GCT TGG TAC CAG CAG AAA CCA GGA CAG
 Y   N   K   M   N   Y   L   A   W   Y   Q   Q   K   P   G   Q>
___a___a___a____TRANSLATION OF 7A3 VL.SEQ [A]__a___a___a___a___>

    150         160         170         180         190
*     *     *     *     *     *     *     *     *     *
CCT CCT AAG CTG CTC ATT AAC TGG GCA TCT ACC CGG GAA TCC GGG GTC
 P   P   K   L   L   I   N   W   A   S   T   R   E   S   G   V>;
___a___a___a____TRANSLATION OF 7A3 VL.SEQ [A]__a___a___a___a___>

       200         210         220         230         240
  *     *     *     *     *     *     *     *     *     *
CCT GAC CGA TTC AGT GGC AGC GGG TCT GGG ACA GAT TTC ACT CTC ACC
 P   D   R   F   S   G   S   G   S   G   T   D   F   T   L   T>
```

```
___a___a___a____TRANSLATION OF 7A3 VL.SEQ [A]__a___a___a___a___>

          250          260          270          280
      *      *      *      *      *      *      *      *      *
ATC AGC AGC CTG CAG GCT GAA GAT GTG GCA GTT TAT TAC TGT CAG CAA
 I   S   S   L   Q   A   E   D   V   A   V   Y   Y   C   Q   Q>
___a___a___a____TRANSLATION OF 7A3 VL.SEQ [A]__a___a___a___a___>

290          300          310          320          330
  *      *      *      *      *      *      *      *      *      *
TAT TAT GCA ACT CCT CTG ACG TTC GGC CAC GGG ACC AAG GTG GAA ATC
 Y   Y   A   T   P   L   T   F   G   H   G   T   K   V   E   I>
___a___a___a____TRANSLATION OF 7A3 VL.SEQ [A]__a___a___a___a___>

  340
    *
AAA CGT (SEQ ID NO: 15)
 K   R> (SEQ ID NO:16)
___a___>
```

FIG. 1(b)(ii) 10A6 VL

Sequence Range: 1 to 357

```
          10           20           30           40
      *      *      *      *      *      *      *      *      *
CAC GTT ATA CTG ACT CAG GAC CCT GCT GTG TCT GTG GCC TTG GGA CAG
 H   V   I   L   T   Q   D   P   A   V   S   V   A   L   G   Q>
___a___a___a____TRANSLATION OF 10A6 VL.SEQ [A]_a___a___a___a___>

50           60           70           80           90
  *      *      *      *      *      *      *      *      *      *
ACA GTC AGG ATC ACG TGC CAA GGA GAC AGC CTC AAA AGC TAC TAT GCA
 T   V   R   I   T   C   Q   G   D   S   L   K   S   Y   Y   A>
___a___a___a____TRANSLATION OF 10A6 VL.SEQ [A]_a___a___a___a___>

  100          110          120          130          140
```

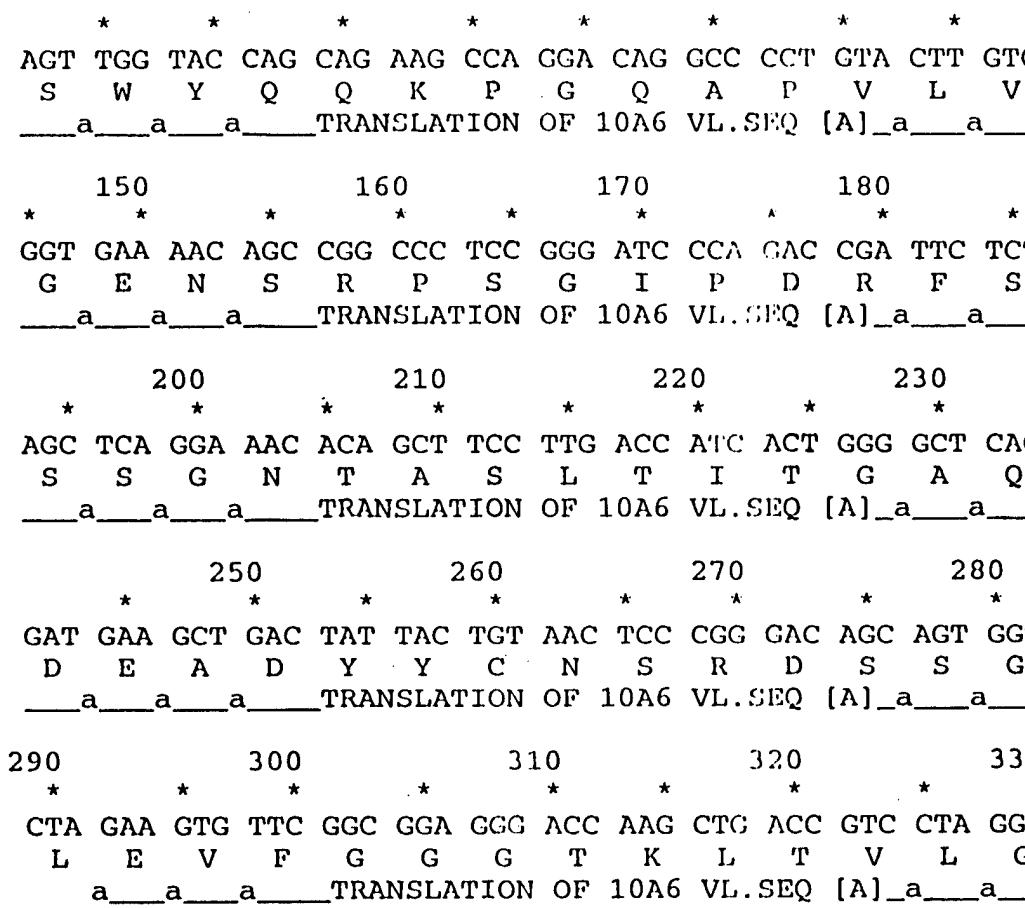
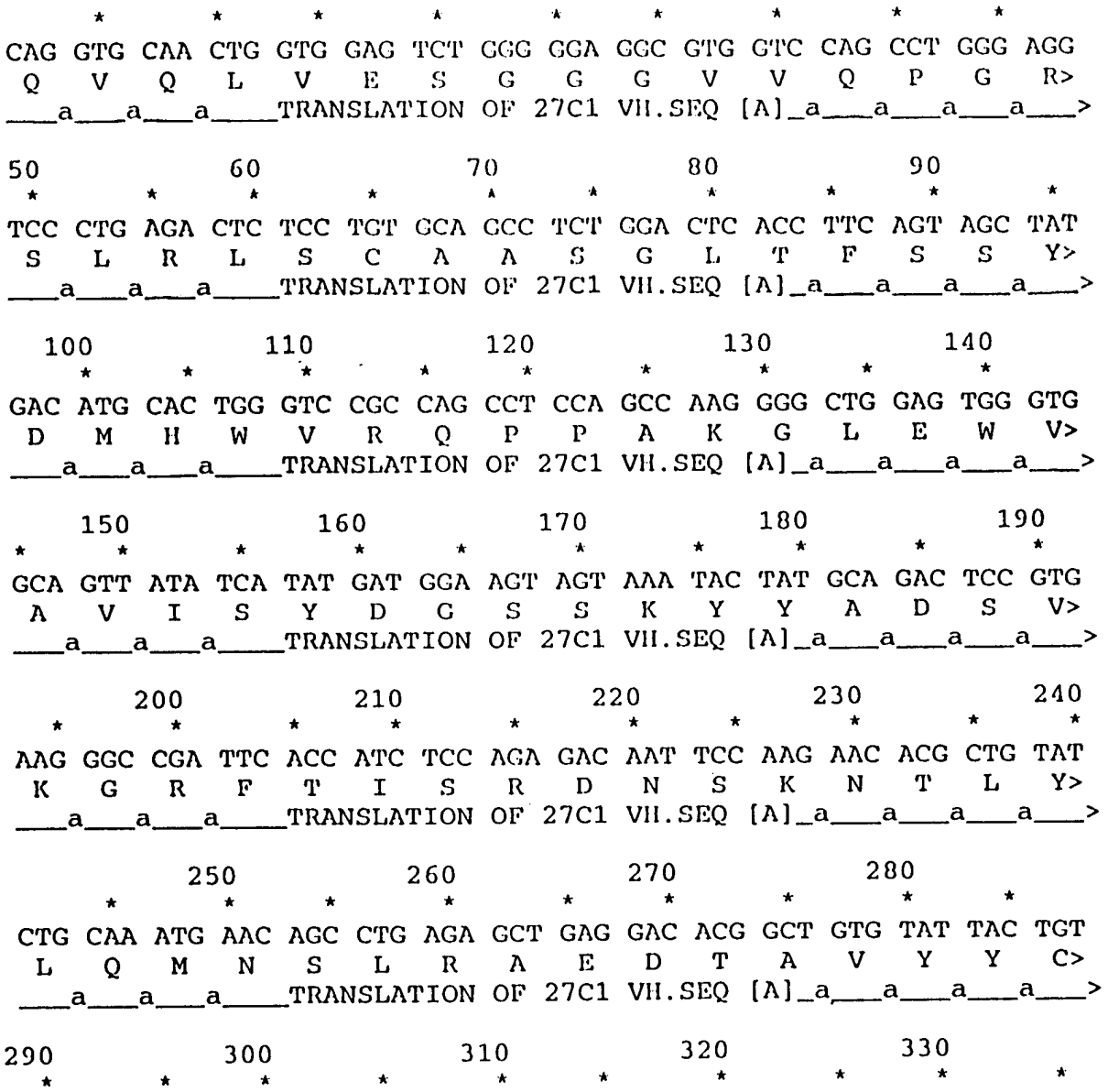


Figure 1 (c) Antibodies to TGFbeta1 isolated from CDR3 spiking experiment

FIG. 1(c) (i) 27C1 VH

Sequence Range: 1 to 369

10 20 30 40


CAG GTG CAA CTG GTG GAG TCT GGG GGA GGC GTG GTC CAG CCT GGG AGG
Q V Q L V E S G G G V V Q P G R>
___a___a___a____TRANSLATION OF 27C1 VH.SEQ [A]_a___a___a___a___>
50 60 70 80 90
TCC CTG AGA CTC TCC TGT GCA GCC TCT GGA CTC ACC TTC AGT AGC TAT
S L R L S C A A S G L T F S S Y>
___a___a___a____TRANSLATION OF 27C1 VH.SEQ [A]_a___a___a___a___>
100 110 120 130 140
GAC ATG CAC TGG GTC CGC CAG CCT CCA GCC AAG GGG CTG GAG TGG GTG
D M H W V R Q P P A K G L E W V>
___a___a___a____TRANSLATION OF 27C1 VH.SEQ [A]_a___a___a___a___>
150 160 170 180 190
GCA GTT ATA TCA TAT GAT GGA AGT AGT AAA TAC TAT GCA GAC TCC GTG
A V I S Y D G S S K Y Y A D S V>
___a___a___a____TRANSLATION OF 27C1 VH.SEQ [A]_a___a___a___a___>
200 210 220 230 240
AAG GGC CGA TTC ACC ATC TCC AGA GAC AAT TCC AAG AAC ACG CTG TAT
K G R F T I S R D N S K N T L Y>
___a___a___a____TRANSLATION OF 27C1 VH.SEQ [A]_a___a___a___a___>
250 260 270 280
CTG CAA ATG AAC AGC CTG AGA GCT GAG GAC ACG GCT GTG TAT TAC TGT
L Q M N S L R A E D T A V Y Y C>
___a___a___a____TRANSLATION OF 27C1 VH.SEQ [A]_a___a___a___a___>
290 300 310 320 330

```
GCG CGA ACT GGT GAA TAT AGT GGC TAC GAC ACG AGT GGT GTG GAG CTC
 A   R   T   G   E   Y   S   G   Y   D   T   S   G   V   E   L>
___a___a___a____TRANSLATION OF 27C1 VH.SEQ [A]_a___a___a___a___>

  340           350           360
    *     *       *       *     *       *
TGG GGG CAA GGG ACC ACG GTC ACC GTC TCC TCA (SEQ ID NO:11)
 W   G   Q   G   T   T   V   T   V   S   S> (SEQ ID NO:12)
___a__TRANSLATION OF 27C1 VH.SEQ [A]___a___>
```

Figure 2 Sequences of antibodies specific for TGFbeta2

(a) Antibodies to TGFbeta 2 isolated directly from repertoires

FIG 2.(a) (i) 2A-H11 VH (also known as 6H1 VH)

Sequence Range: 1 to 345

```
          10          20          30          40
     *    *    *     *    *     *    *     *    *
GAG GTG CAG CTG GTG GAG TCT GGG GGA GGC GTG GTC CAG CCT GGG AGG
 E   V   Q   L   V   E   S   G   G   G   V   V   Q   P   G   R>
___a___a___a____TRANSLATION OF 6H1 VH.SEQ [A]__a___a___a___a___>

50          60          70          80          90
 *     *     *     *     *     *     *     *     *     *
TCC CTG AGA CTC TCC TGT GCA GCG TCT GGA TTC ACC TTC AGT AGC TAT
 S   L   R   L   S   C   A   A   S   G   F   T   F   S   S   Y>
___a___a___a____TRANSLATION OF 6H1 VH.SEQ [A]__a___a___a___a___>

  100         110         120         130         140
    *     *     *     *     *     *     *     *     *
GGC ATG CAC TGG GTC CGC CAG GCT CCA GGC AAG GGG CTG GAG TGG GTG
 G   M   H   W   V   R   Q   A   P   G   K   G   L   E   W   V>
___a___a___a____TRANSLATION OF 6H1 VH.SEQ [A]__a___a___a___a___>

    150         160         170         180         190
*     *     *     *     *     *     *     *     *     *
GCA GTT ATA TGG TAT GAT GGA AGT AAT AAA TAC TAT GCA GAC TCC GTG
 A   V   I   W   Y   D   G   S   N   K   Y   Y   A   D   S   V>
___a___a___a____TRANSLATION OF 6H1 VH.SEQ [A]__a___a___a___a___>

      200         210         220         230         240
  *     *     *     *     *     *     *     *     *     *
AAG GGC CGA TTC ACC ATC TCC AGA GAC AAT TCC AAG AAC ACG CTG TAT
 K   G   R   F   T   I   S   R   D   N   S   K   N   T   L   Y>
___a___a___a____TRANSLATION OF 6H1 VH.SEQ [A]__a___a___a___a___>
```

```
          250          260          270          280
      *    *    *    *    *    *    *    *    *
CTG CAA ATG GAC AGC CTG AGA GCC GAG GAC ACG GCC GTG TAT TAC TGT
 L   Q   M   D   S   L   R   A   E   D   T   A   V   Y   Y   C>
___a___a___a____TRANSLATION OF 6H1 VH.SEQ [A]__a___a___a___a___>

290          300          310          320          330
 *    *    *    *    *    *    *    *    *    *
GGA AGA ACG CTG GAG TCT AGT TTG TGG GGC CAA GGC ACC CTG GTC ACC
 G   R   T   L   E   S   S   L   W   G   Q   G   T   L   V   T>
___a___a___a____TRANSLATION OF 6H1 VH.SEQ [A]__a___a___a___a___>

  340
   *    *
GTC TCC TCA  (SEQ ID NO:5)
 V   S   S>  (SEQ ID NO:6)
___a___a___>
```

FIG 2.(a)(ii) 2A-A9 (also known as 11E6 VH)

Sequence Range: 1 to 350

```
          10           20           30           40
      *    *    *    *    *    *    *    *    *
GAG ATT CAG CTG GTG GAG TCT GGG GGA GGC GTG GTC CAG CCT GGG AGA
 E   I   Q   L   V   E   S   G   G   G   V   V   Q   P   G   R>
___a___a___a____TRANSLATION OF 11E6 VH.SEQ [A]_a___a___a___a___>

50           60           70           80           90
 *    *    *    *    *    *    *    *    *    *
TCC CTG AGA CTC TCC TGT GCA GCC TCT GGA TTC ACC TTC AGT AGC TAT
 S   L   R   L   S   C   A   A   S   G   F   T   F   S   S   Y>
___a___a___a____TRANSLATION OF 11E6 VH.SEQ [A]_a___a___a___a___>

  100          110          120          130          140
   *    *    *    *    *    *    *    *    *
```

```
GCT ATG CAC TGG GTC CGC CAG GCT CCA GCC AAG GGG CTG GAG TGG GTG
 A   M   H   W   V   R   Q   A   P   A   K   G   L   E   W   V>
___a___a___a____TRANSLATION OF 11E6 VH.SEQ [A]_a___a___a___a___>

    150           160           170           180           190
*     *       *     *     *     *     *     *     *     *     *
GCA GTT ATA TCA TAT GAT GGA AGC AAT AAA TAC TAC GCA GAC TCC GTG
 A   V   I   S   Y   D   G   S   N   K   Y   Y   A   D   S   V>
___a___a___a____TRANSLATION OF 11E6 VH.SEQ [A]_a___a___a___a___>

        200           210           220           230           240
  *     *       *     *     *     *     *     *     *     *     *
AAG GGC CGA TTC ACC ATC TCC AGA GAC AAT TCC AAG AAC ACG CTG TAT
 K   G   R   F   T   I   S   R   D   N   S   K   N   T   L   Y>
___a___a___a____TRANSLATION OF 11E6 VH.SEQ [A]_a___a___a___a___>

          250           260           270           280
     *     *     *     *     *     *     *     *     *
CTG CAA ATG AAC AGC CTG AGA GCT GAG GAC ACG GCC GTG TAT TAC TGT
 L   Q   M   N   S   L   R   A   E   D   T   A   V   Y   Y   C>
___a___a___a____TRANSLATION OF 11E6 VH.SEQ [A]_a___a___a___a___>

290           300           310           320           330
  *     *     *     *     *     *     *     *     *     *
GCA AGA GCG GGG TTG GAA ACG ACG TGG GGC CAA GGA ACC CTG GTC ACC
 A   R   A   G   L   E   T   T   W   G   Q   G   T   L   V   T>
___a___a___a____TRANSLATION OF 11E6 VH.SEQ [A]_a___a___a___a___>

  340           350
    *     *     *
GTC TCC TCA AGT GG   (SEQ ID NO:36)
 V   S   S   S   G>  (SEQ ID NO:37)
___TRANSLATION_a__>
```

FIG 2.(a)(iii) Gold11-VH

Sequence Range: 1 to 369

```
          10          20          30          40
      *   *   *   *   *   *   *   *   *
CAG GTC ACC TTG AAG GAG TCT GGG GGA AGC GTG GTC CAG CCT GGG AGG
 Q   V   T   L   K   E   S   G   G   S   V   V   Q   P   G   R>
___a___a___a___a_TRANSLATION OF GOLD11-VH [A]__a___a___a___a___>

50          60          70          80          90
 *   *   *   *   *   *   *   *   *   *   *
TCC CTG AGA CTC TCC TGT GCA GCC TCT GGA TTC ACC TTC AGT AGC TAT
 S   L   R   L   S   C   A   A   S   G   F   T   F   S   S   Y>
___a___a___a___a_TRANSLATION OF GOLD11-VH [A]__a___a___a___a___>

 100         110         120         130         140
   *   *   *   *   *   *   *   *   *   *
GGC ATG CAC TGG GTC CGC CAG GCT CCA GGC AAG GGG CTG GAG TGG GTG
 G   M   H   W   V   R   Q   A   P   G   K   G   L   E   W   V>
___a___a___a___a_TRANSLATION OF GOLD11-VH [A]__a___a___a___a___>

    150         160         170         180         190
*   *   *   *   *   *   *   *   *   *   *   *
GCA GTT ATA TCA TAT GAT GGA AGT AAT AAA TAC TAT GCA GAC TCC GTG
 A   V   I   S   Y   D   G   S   N   K   Y   Y   A   D   S   V>
___a___a___a___a_TRANSLATION OF GOLD11-VH [A]__a___a___a___a___>

        200         210         220         230         240
  *   *   *   *   *   *   *   *   *   *   *   *
AAG GGC CGA TTC ACC ATC TCC AGA GAC AAT TCC AAG AAC ACG CAG TAT
 K   G   R   F   T   I   S   R   D   N   S   K   N   T   Q   Y>
___a___a___a___a_TRANSLATION OF GOLD11-VH [A]__a___a___a___a___>

          250         260         270         280
```

```
     *       *       *       *       *       *       *       *       *
CTG CAA ATG AAC AGC CTG AGA GCT GAA GAC ACG GCA GAG TAT TAC TGT
 L   Q   M   N   S   L   R   A   E   D   T   A   E   Y   Y   C>
___a___a___a___a_TRANSLATION OF GOLD11-VH [A]__a___a___a___a___>

290           300           310           320           330
 *       *     *       *     *       *     *       *     *       *
GCG AGA ACT GGG GAA TAT AGT GGC CAC GCA TCT ACT GGA GAG AAC GTC
 A   R   T   G   E   Y   S   G   H   A   S   T   G   E   N   V>
___a___a___a___a_TRANSLATION OF GOLD11-VH [A]__a___a___a___a___>

  340           350           360
    *       *     *       *     *       *
TGG GGC CGG GGC ACC CTG GTC ACC GTC TCG AGT  (SEQ ID NO:115)
 W   G   R   G   T   L   V   T   V   S   S>  (SEQ ID NO:116)
___a___TRANSLATION OF GOLD11-VH [A]____a___>
```

FIG 2.(a)(iv) Gold11-VL

Sequence Range: 1 to 336

```
                10            20            30            40
     *       *     *       *     *       *     *       *     *
TCC TAT GTG CTG ACT CAC CCC CCC TCA GTG TCT GGG ACC CCC GGG CAG
 S   Y   V   L   T   H   P   P   S   V   S   G   T   P   G   Q>
___a___a___a___a_TRANSLATION OF GOLD11-VL [A]__a___a___a___a___>

50            60            70            80            90
 *       *     *       *     *       *     *       *     *       *
AGA GTC ACC ATC TCT TGT TCT GGA GGC AGA TCC AAC ATC GGC AGT AAT
 R   V   T   I   S   C   S   G   G   R   S   N   I   G   S   N>
___a___a___a___a_TRANSLATION OF GOLD11-VL [A]__a___a___a___a___>

  100           110           120           130           140
    *       *     *       *     *       *     *       *     *
ACT GTA AAG TGG TAT CAG CAG CTC CCA GGA ACG CCC CCC AAA CTC CTC
 T   V   K   W   Y   Q   Q   L   P   G   T   P   P   K   L   L>
```

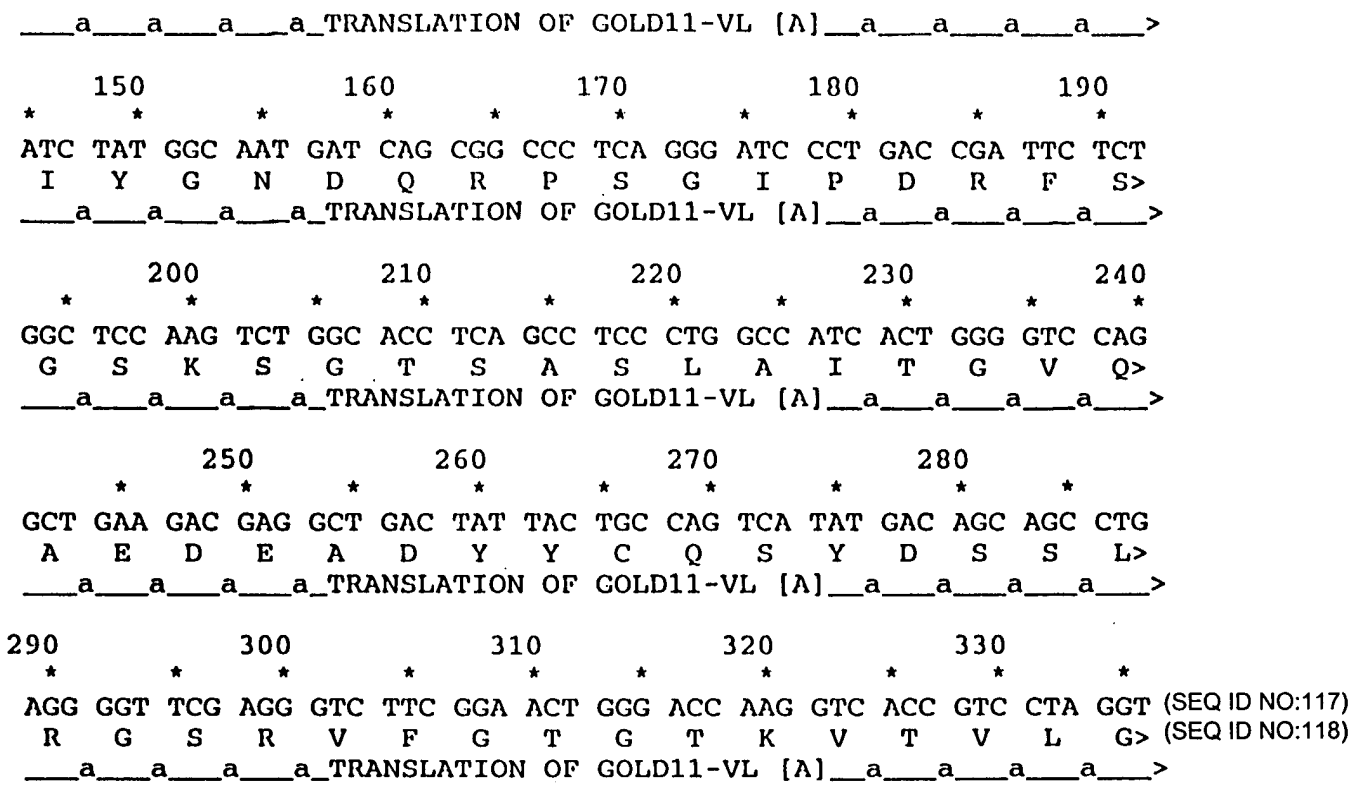
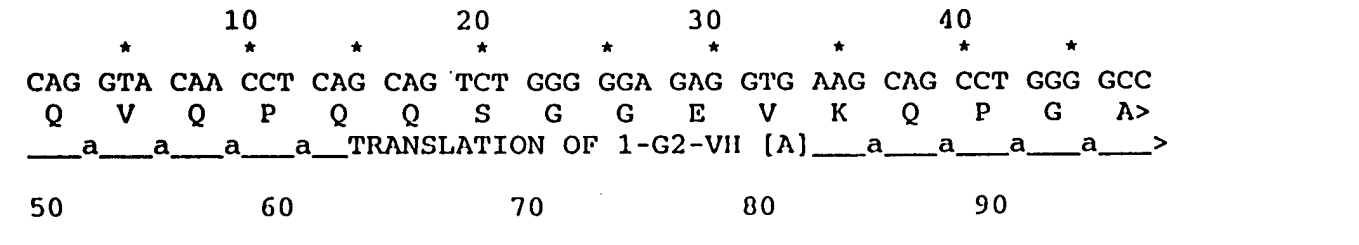
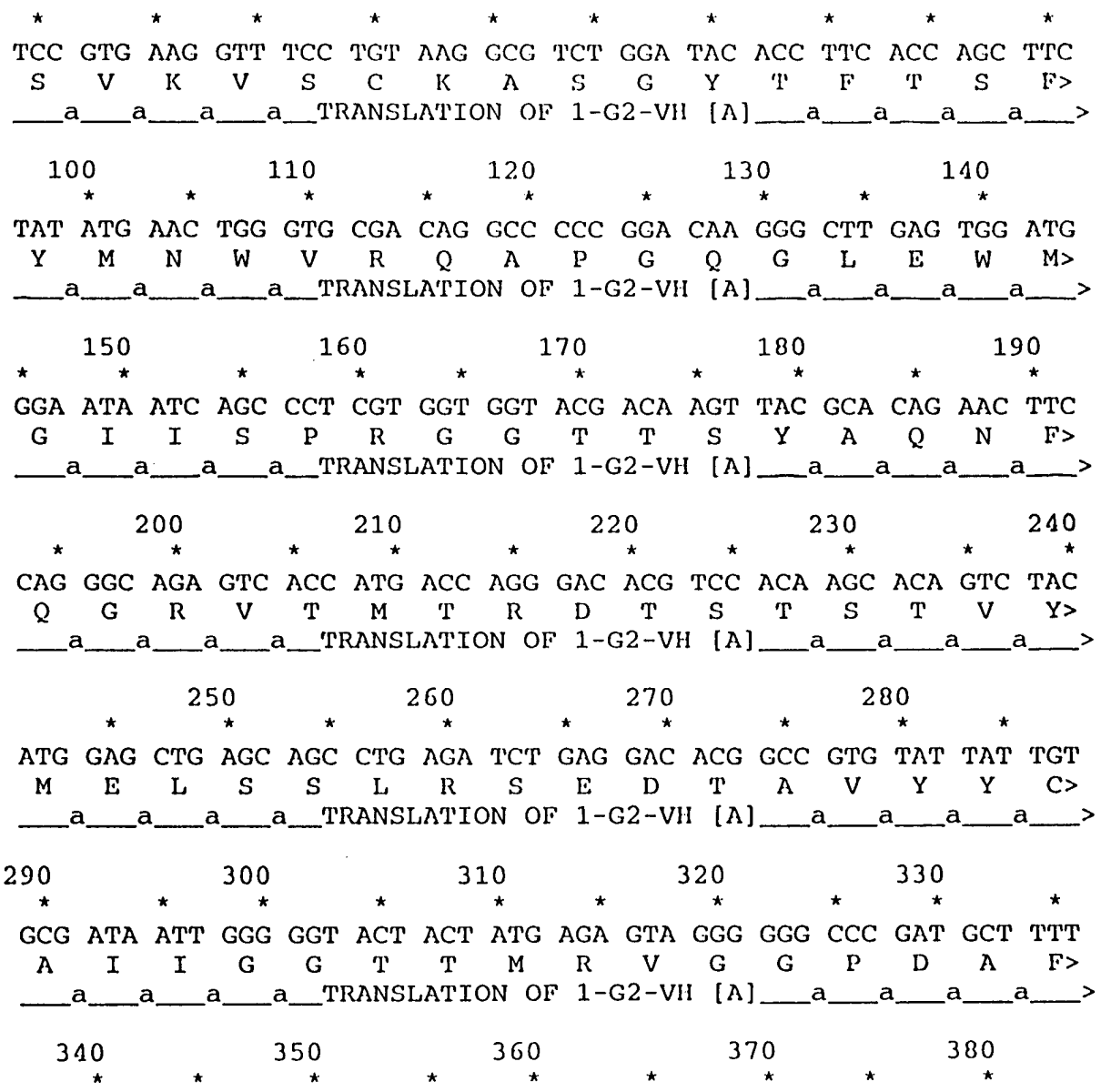


FIG 2.(a)(v)

1-G2

Sequence Range: 1 to 381




TCC GTG AAG GTT TCC TGT AAG GCG TCT GGA TAC ACC TTC ACC AGC TTC
S V K V S C K A S G Y T F T S F>
___a___a___a___a__TRANSLATION OF 1-G2-VH [A]___a___a___a___a___>
100 110 120 130 140
TAT ATG AAC TGG GTG CGA CAG GCC CCC GGA CAA GGG CTT GAG TGG ATG
Y M N W V R Q A P G Q G L E W M>
___a___a___a___a__TRANSLATION OF 1-G2-VH [A]___a___a___a___a___>
150 160 170 180 190
GGA ATA ATC AGC CCT CGT GGT GGT ACG ACA AGT TAC GCA CAG AAC TTC
G I I S P R G G T T S Y A Q N F>
___a___a___a___a__TRANSLATION OF 1-G2-VH [A]___a___a___a___a___>
200 210 220 230 240
CAG GGC AGA GTC ACC ATG ACC AGG GAC ACG TCC ACA AGC ACA GTC TAC
Q G R V T M T R D T S T S T V Y>
___a___a___a___a__TRANSLATION OF 1-G2-VH [A]___a___a___a___a___>
250 260 270 280
ATG GAG CTG AGC AGC CTG AGA TCT GAG GAC ACG GCC GTG TAT TAT TGT
M E L S S L R S E D T A V Y Y C>
___a___a___a___a__TRANSLATION OF 1-G2-VH [A]___a___a___a___a___>
290 300 310 320 330
GCG ATA ATT GGG GGT ACT ACT ATG AGA GTA GGG GGG CCC GAT GCT TTT
A I I G G T T M R V G G P D A F>
___a___a___a___a__TRANSLATION OF 1-G2-VH [A]___a___a___a___a___>
340 350 360 370 380

```
GAT ATC TGG GGC CAA GGG ACA ATG GTC ACC GTC ACC GTC TCT TCA (SEQ ID NO:119)
 D   I   W   G   Q   G   T   M   V   T   V   T   V   S   S> (SEQ ID NO:120)
___a___a___a____TRANSLATION OF 1-G2-VH [A]_a___a___a___a___>
```

FIG 2.(a)(vi)

1-H6

Sequence Range: 1 to 381

```
          10          20          30          40
     *    *    *      *    *      *    *      *    *
GAG GTG CAG CTG GTG GAG TCT GGG GGA GGC GTG GTC CAG CCT GGG AGG
 E   V   Q   L   V   E   S   G   G   G   V   V   Q   P   G   R>
___a___a___a___a__TRANSLATION OF 1-H6 VH [A]___a___a___a___a___>

50          60          70          80          90
 *     *    *     *     *     *     *     *     *     *
TCC CTG AGA CTC TCC TGT GCA GCG TCT GGA TTC ACC TTC AGG AAC TAT
 S   L   R   L   S   C   A   A   S   G   F   T   F   R   N   Y>
___a___a___a___a__TRANSLATION OF 1-H6 VH [A]___a___a___a___a___>

  100         110         120         130         140
    *     *     *     *     *     *     *     *     *
GGC ATG CAC TGG GTC CGC CAG GCT CCA GGC AAG GGG CTG GAG TGG GTG
 G   M   H   W   V   R   Q   A   P   G   K   G   L   E   W   V>
___a___a___a___a__TRANSLATION OF 1-H6 VH [A]___a___a___a___a___>

    150         160         170         180         190
*     *     *     *     *     *     *     *     *     *
GCA GTT ATA TGG TAT GAT GGA AGT AAT AAA TAC TAT GCA GAC TCC GTG
 A   V   I   W   Y   D   G   S   N   K   Y   Y   A   D   S   V>
___a___a___a___a__TRANSLATION OF 1-H6 VH [A]___a___a___a___a___>

       200         210         220         230         240
  *     *     *     *     *     *     *     *     *     *
AAG GGC CGA TTC ACC ATC TCC AGA GAC AAT TCC AAG AAC ACG CTG TAT
```

```
  K   G   R   F   T   I   S   R   D   N   S   K   N   T   L   Y>
___a___a___a___a__TRANSLATION OF 1-H6 VH [A]___a___a___a___a___>

          250           260           270           280
      *       *       *       *       *       *       *       *
CTG CAA ATG AAC AGC CTG AGA GTC GAG GAC ACG GCT GTT TAT TAC TGT
 L   Q   M   N   S   L   R   V   E   D   T   A   V   Y   Y   C>
___a___a___a___a__TRANSLATION OF 1-H6 VH [A]___a___a___a___a___>

290           300           310           320           330
  *       *       *       *       *       *       *       *       *
GCG AGA AGA TGG TAT GGT GGC AGT GGT TAT TGG GGC CAC TTC TAC TCC
 A   R   R   W   Y   G   G   S   G   Y   W   G   H   F   Y   S>
___a___a___a___a__TRANSLATION OF 1-H6 VH [A]___a___a___a___a___>

  340           350           360           370           380
    *       *       *       *       *       *       *       *
TAC ATG GAC GGC TGG GGC AAA GGG ACC AAG GTC ACC GTC TCC TCA (SEQ ID NO:121)
 Y   M   D   G   W   G   K   G   T   K   V   T   V   S   S> (SEQ ID NO:122)
___a___a___a____TRANSLATION OF 1-H6 VH [A]_a___a___a___a___>
```

Figure 2(b)(i)

```
            10          20          30          40
GAT GTT GTG ATG ACT CAG TCT CCA TCC TCC CTG TCT GCA TCT GTA GGA
 D   V   V   M   T   Q   S   P   S   S   L   S   A   S   V   G>

50          60          70          80          90
GAC AGA GTC ACC ATC ACT TGC CGG GCC AGT CAG GGC ATT AGC AAT TAT
 D   R   V   T   I   T   C   R   A   S   Q   G   I   S   N   Y>

 100         110         120         130         140
TTA GCC TGG TAT CAG CAA AAA CCA GGG AAA GCC CCT AAG CTC CTG ATC
 L   A   W   Y   Q   Q   K   P   G   K   A   P   K   L   L   I>

   150         160         170         180         190
TAT AAG GCA TCT ACT TTA GAA AGT GGG GTC CCA TCA AGG TTC AGT GGC
 Y   K   A   S   T   L   E   S   G   V   P   S   R   F   S   G>

       200         210         220         230         240
AGT GGA TCT GGG ACA GAA TTC ACT CTC ACA ATC AGC AGT CTG CAA CCT
 S   G   S   G   T   E   F   T   L   T   I   S   S   L   Q   P>

           250         260         270         280
GAA GAT TTT GCA ACT TAC TAC TGT CAA CAG AGT TAC AGT ACC CCT CGA
 E   D   F   A   T   Y   Y   C   Q   Q   S   Y   S   T   P   R>

290         300         310         320         330
ACG TTC GGC CAA GGG ACC AAA GTG GAT ATC AAA CGT   (SEQ ID NO:38)
 T   F   G   Q   G   T   K   V   D   I   K   R   (SEQ ID NO:39)
```

Figure 2(b)(ii)

```
                10                  20                  30                  40
TCG TCT GAG CTG ACT CAG GAC CCT GCT GTG TCT GTG GCC TTG GGA CAG
 S   S   E   L   T   Q   D   P   A   V   S   V   A   L   G   Q>

50                  60                  70                  80                  90
ACA GTC AGG ATC ACA TGC CAA GGA GAC AGC CTC AGA AGC TAT TAT GCA
 T   V   R   I   T   C   Q   G   D   S   L   R   S   Y   Y   A>

  100                 110                 120                 130                 140
AGC TGG TAC CAG CAG AAG CCA GGA CAG GCC CCT GTA CTT GTC ATC TAT
 S   W   Y   Q   Q   K   P   G   Q   A   P   V   L   V   I   Y>

    150                 160                 170                 180                 190
GGT AAA AAC AAC CGG CCC TCA GGG ATC CCA GAC CGA TTC GCT GGC TCC
 G   K   N   N   R   P   S   G   I   P   D   R   F   A   G   S>

        200                 210                 220                 230                 240
AAC TCA GGA AAC ACA GCT TCC TTG ACC ATC ACT GGG GCT CAG GCG GAG
 N   S   G   N   T   A   S   L   T   I   T   G   A   Q   A   E>

            250                 260                 270                 280
GAT GAG GCT GAC TAT TAC TGT AGC TCC CGG GAC AGC AGT GGT AAC CAT
 D   E   A   D   Y   Y   C   S   S   R   D   S   S   G   N   H>

290                 300                 310                 320
GTG GTT TTC GGC GGA GGG ACC AAG CTG ACC GTC CTA GGT (SEQ ID NO:40)
 V   V   F   G   G   G   T   K   L   T   V   L   G> (SEQ ID NO:41)
```

Figure 2(b)(iii)

```
                10                  20                  30                  40
TCG TCT GAG CTG ACT CAG GAC CCT GCT GTG TCT GTG GCC TTG GGA CAG
 S   S   E   L   T   Q   D   P   A   V   S   V   A   L   G   Q>

50                  60                  70                  80                  90
ACA GTC AGG ATC ACA TGC CAA GGA GAC AGC CTC AGA AGC TAT TAT GCA
 T   V   R   I   T   C   Q   G   D   S   L   R   S   Y   Y   A>

  100                 110                 120                 130                 140
AGC TGG TAC CAG CAG AAG CCA GGA CAG GCC CCT GTA CTT GTC ATC TAT
 S   W   Y   Q   Q   K   P   G   Q   A   P   V   L   V   I   Y>

    150                 160                 170                 180                 190
GGT AAA AAC AAC CGG CCC TCA GGG ATC CCA GAC CGA TTC TCT GGC TCC
 G   K   N   N   R   P   S   G   I   P   D   R   F   S   G   S>

        200                 210                 220                 230                 240
AGC TCA GGA AAC ACA GCT TCC TTG ACC ATC ACT GGG GCT CAG GCG GAA
 S   S   G   N   T   A   S   L   T   I   T   G   A   Q   A   E>

            250                 260                 270                 280
GAT GAG GCT GAC TAT TAC TGT AAC TCC CGG GAC AGC AGT AGT ACC CAT
 D   E   A   D   Y   Y   C   N   S   R   D   S   S   S   T   H>

290                 300                 310                 320                 330
CGA GGG GTG TTC GGC GGA GGG ACC AAG CTG ACC GTC CTA GGT (SEQ ID NO:42)
 R   G   V   F   G   G   G   T   K   L   T   V   L   G (SEQ ID NO:43)
```

Figure 2(b)(iv)

```
                10                  20                  30                  40
GAA GTT GTG CTG ACT CAG TCT CCA TCC TCC CTG TCT GCA TCT GTA GGA
 E   V   V   L   T   Q   S   P   S   S   L   S   A   S   V   G>

50                  60                  70                  80                  90
GAC AGA GTC ACC ATC ACT TGC CGG GCA AGT CAG GGC ATT GGA GAT GAT
 D   R   V   T   I   T   C   R   A   S   Q   G   I   G   D   D>

  100                 110                 120                 130                 140
TTG GGC TGG TAT CAG CAG AAG CCA GGG AAA GCC CCT ATC CTC CTG ATC
 L   G   W   Y   Q   Q   K   P   G   K   A   P   I   L   L   I>

    150                 160                 170                 180                 190
TAT GGT ACA TCC ACT TTA CAA AGT GGG GTC CCG TCA AGG TTC AGC GGC
 Y   G   T   S   T   L   Q   S   G   V   P   S   R   F   S   G>

        200                 210                 220                 230                 240
AGT GGA TCT GGC ACA GAT TTC ACT CTC ACC ATC AAC AGC CTG CAG CCT
 S   G   S   G   T   D   F   T   L   T   I   N   S   L   Q   P>

            250                 260                 270                 280
GAA GAT TTT GCA ACT TAT TAC TGT CTA CAA GAT TCC AAT TAC CCG CTC
 E   D   F   A   T   Y   Y   C   L   Q   D   S   N   Y   P   L>

290                 300                 310                 320
ACT TTC GGC GGA GGG ACA CGA CTG GAG ATT AAA CGT (SEQ ID NO:44)
 T   F   G   G   G   T   R   L   E   I   K   R (SEQ ID NO:45)
```

Figure 2(b)(v)

```
          10          20          30          40
TCG TCT GAG CTG ACT CAG GAC CCT GCT GTG TCT GTG GCC TTG GGA CAG
 S   S   E   L   T   Q   D   P   A   V   S   V   A   L   G   Q>

50          60          70          80          90
ACA GTC AGG ATC ACA TGC CAA GGA GAC AGC CTC AGA AAC TAT TAT GCA
 T   V   R   I   T   C   Q   G   D   S   L   R   N   Y   Y   A>

  100         110         120         130         140
AAC TGG TAC CAG CAG AAG CCA GGA CAG GCC CCT GTA CTT GTC ATC TAT
 N   W   Y   Q   Q   K   P   G   Q   A   P   V   L   V   I   Y>

    150         160         170         180         190
GGT AAA AAC AAC CGG CCC TCA GGG ATC CCA GAC CGA TTC TCT GGC TCC
 G   K   N   N   R   P   S   G   I   P   D   R   F   S   G   S>

        200         210         220         230         240
AGC TCA GGG AAC ACA GCT TCC TTG ACC ATC ACT GGG GCT CGG GCG GAA
 S   S   G   N   T   A   S   L   T   I   T   G   A   R   A   E>

          250         260         270         280
GAT GAG GGT GTC TAT TAC TGT AAC TCC CGG GAC AGC AGT GGT GCG GTT
 D   E   G   V   Y   Y   C   N   S   R   D   S   S   G   A   V>

290         300         310         320
TTC GGC GGA GGG ACC AAG CTG ACC GTC CTA GGT (SEQ ID NO:46)
 F   G   G   G   T   K   L   T   V   L   G (SEQ ID NO:47)
```

FIG. 2(b)(vi)

6H1_VL

Sequence Range: 1 to 324

```
          10          20          30          40
     *    *    *    *    *    *    *    *    *
GAA GTT GTG CTG ACT CAG TCT CCA TCC TCC CTG TCT GCA TCT GTA GGA
 E   V   V   L   T   Q   S   P   S   S   L   S   A   S   V   G>
___a___a___a____TRANSLATION OF 11E6 VL.SEQ [A]_a___a___a___a___>

 50          60          70          80          90
 *    *    *    *    *    *    *    *    *    *
GAC AGA GTC ACC ATC ACT TGC CGG GCA AGT CAG GGC ATT GGA GAT GAT
 D   R   V   T   I   T   C   R   A   S   Q   G   I   G   D   D>
___a___a___a____TRANSLATION OF 11E6 VL.SEQ [A]_a___a___a___a___>

  100         110         120         130         140
    *    *    *    *    *    *    *    *    *    *
TTG GGC TGG TAT CAG CAG AAG CCA GGG AAA GCC CCT ATC CTC CTG ATC
 L   G   W   Y   Q   Q   K   P   G   K   A   P   I   L   L   I>
___a___a___a____TRANSLATION OF 11E6 VL.SEQ [A]_a___a___a___a___>

    150         160         170         180         190
*    *    *    *    *    *    *    *    *    *    *
TAT GGT ACA TCC ACT TTA CAA AGT GGG GTC CCG TCA AGG TTC AGC GGC
 Y   G   T   S   T   L   Q   S   G   V   P   S   R   F   S   G>
___a___a___a____TRANSLATION OF 11E6 VL.SEQ [A]_a___a___a___a___>

       200         210         220         230         240
  *    *    *    *    *    *    *    *    *    *    *    *
AGT GGA TCT GGC ACA GAT TTC ACT CTC ACC ATC AAC AGC CTG CAG CCT
 S   G   S   G   T   D   F   T   L   T   I   N   S   L   Q   P>
___a___a___a____TRANSLATION OF 11E6 VL.SEQ [A]_a___a___a___a___>

          250         260         270         280
     *    *    *    *    *    *    *    *    *    *
GAA GAT TTT GCA ACT TAT TAC TGT CTA CAA GAT TCC AAT TAC CCG CTC
 E   D   F   A   T   Y   Y   C   L   Q   D   S   N   Y   P   L>
___a___a___a____TRANSLATION OF 11E6 VL.SEQ [A]_a___a___a___a___>

290         300         310         320
  *    *    *    *    *    *    *
ACT TTC GGC GGA GGG ACA CGA CTG GAG ATT AAA CGT
 T   F   G   G   G   T   R   L   E   I   K   R>
___a____TRANSLATION OF 11E6 VL.SEQ [A]_a___a___>
```

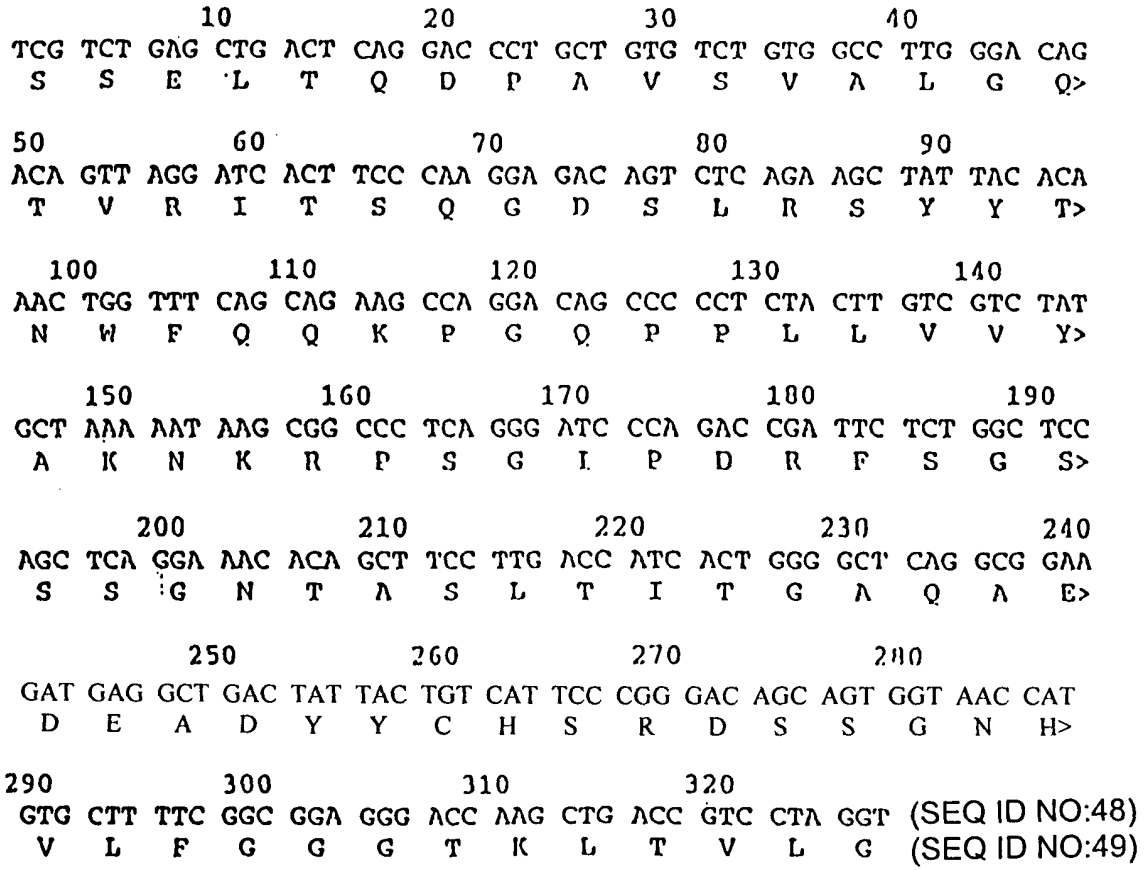
(SEQ ID NO:123)
(SEQ ID NO:124)

(SEQ ID NOS: 19-35)

PARENT (1-B2)	A R T G E Y S G Y D S S G V D V W
27-C1	A R T G E Y S G Y D T S G V E L W
27-D7	A R T R E Y S G H D S S G V D D W
27-E10	A R T G P F S G Y D S S G E D V R
27-H1	A R T E E Y S G Y D S S G V D V W
27-E2	A Q T R E Y T G Y D S S G V D V W
28-A11	A R T E E Y S G F D S T G E D V W
28-E12	A R T E E F S G Y D S S G V D V W
28-H10	A R T G E Y S G Y H S S G V D V R
31-G2	A R T E E F S G Y D S S G V D V W
30-B6	A R A G P F S G Y D S S G E D V R
30-E9	A R T G P F S G Y D S S G E D V W
30-F6	A R T E E F S G Y D S S G V D V W
30-D2	A R T G E Y S G Y D S S G E L V W
31-A2	A R T E E F S G Y D S T G E E V W
31-E11	A R T E E F S G Y D S S G V D V W
31-F1	A R T G E Y S G Y D S S G E D V W

FIGURE 3

Figure 4


10 20 30 40
TCG TCT GAG CTG ACT CAG GAC CCT GCT GTG TCT GTG GCC TTG GGA CAG
S S E L T Q D P A V S V A L G Q>
50 60 70 80 90
ACA GTT AGG ATC ACT TCC CAA GGA GAC AGT CTC AGA AGC TAT TAC ACA
T V R I T S Q G D S L R S Y Y T>
100 110 120 130 140
AAC TGG TTT CAG CAG AAG CCA GGA CAG CCC CCT CTA CTT GTC GTC TAT
N W F Q Q K P G Q P P L L V V Y>
150 160 170 180 190
GCT AAA AAT AAG CGG CCC TCA GGG ATC CCA GAC CGA TTC TCT GGC TCC
A K N K R P S G I P D R F S G S>
200 210 220 230 240
AGC TCA GGA AAC ACA GCT TCC TTG ACC ATC ACT GGG GCT CAG GCG GAA
S S G N T A S L T I T G A Q A E>
250 260 270 280
GAT GAG GCT GAC TAT TAC TGT CAT TCC CGG GAC AGC AGT GGT AAC CAT
D E A D Y Y C H S R D S S G N H>
290 300 310 320
GTG CTT TTC GGC GGA GGG ACC AAG CTG ACC GTC CTA GGT (SEQ ID NO:48)
V L F G G G T K L T V L G (SEQ ID NO:49)

(SEQ ID NOS: 50-52)

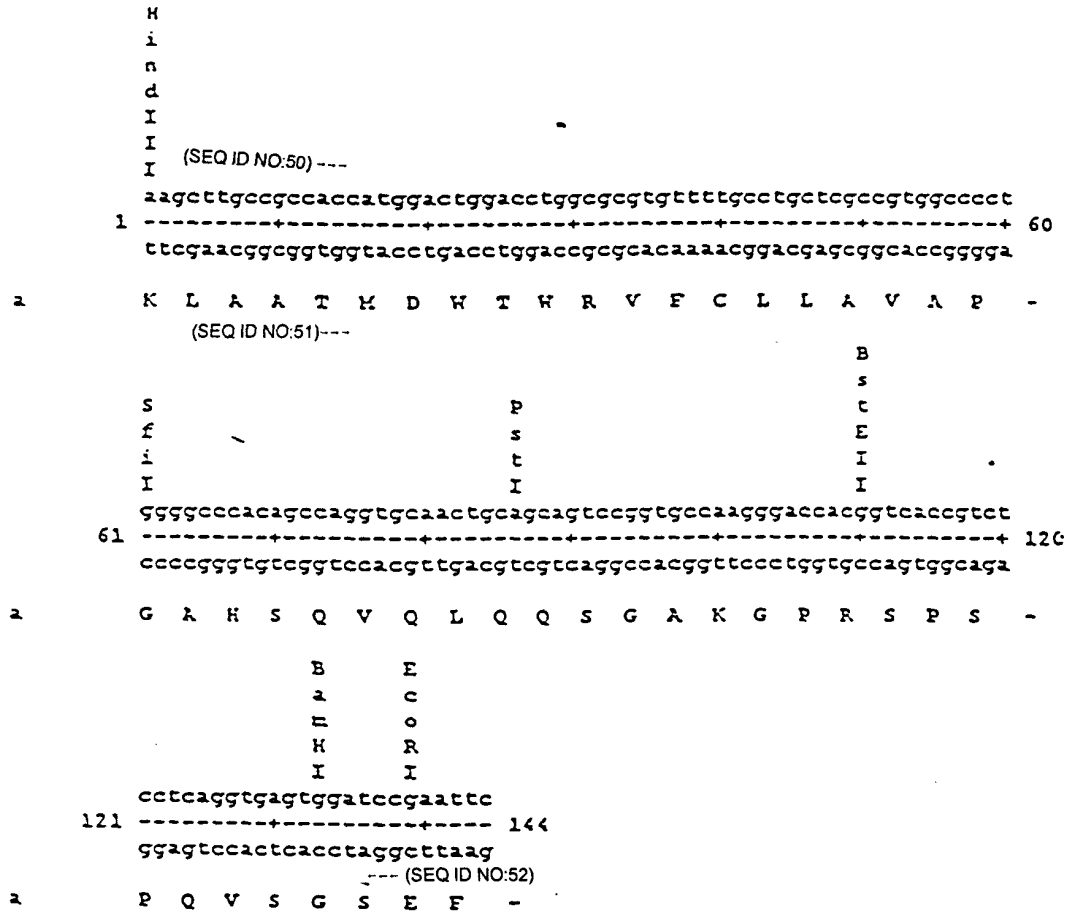
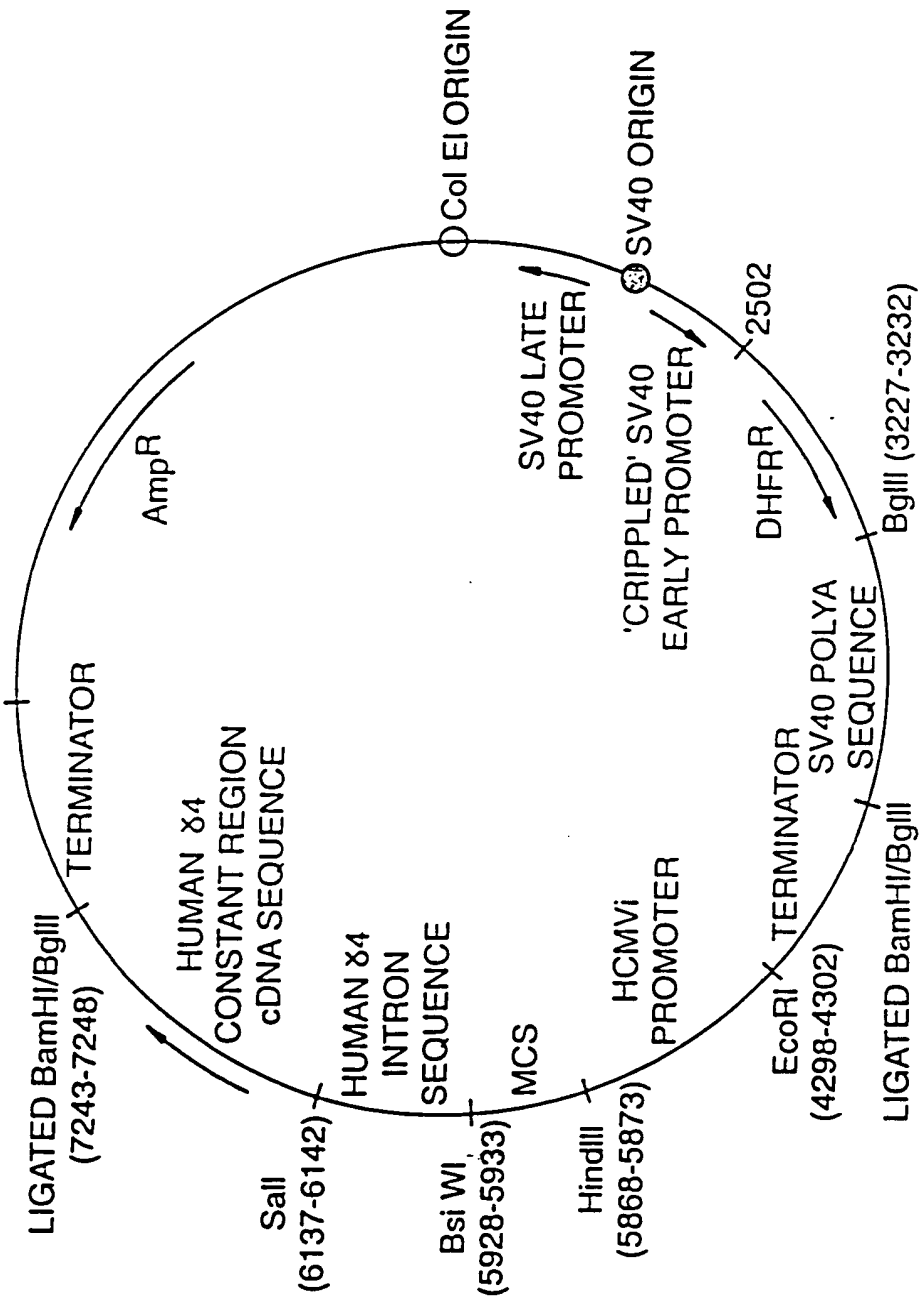


FIGURE 5

Fig.6.


(LIGATED ApoI/EcoRI SITES)
7459/1
LIGATED BamHI/BglII
(7243-7248)
TERMINATOR
AmpR
ColE1 ORIGIN
SV40 ORIGIN
SV40 LATE
PROMOTER
'CRIPPLED' SV40
EARLY PROMOTER
2502
DHFRR
BglII (3227-3232)
HUMAN κ4
CONSTANT REGION
cDNA SEQUENCE
HUMAN κ4
INTRON
SEQUENCE
MCS
HCMVi
PROMOTER
EcoRI
(4298-4302)
TERMINATOR
SV40 POLYA
SEQUENCE
LIGATED BamHI/BglII
(4074-4079)
SalI
(6137-6142)
BsiWI
(5928-5933)
HindIII
(5868-5873)

(SEQ ID NOS: 53-57)

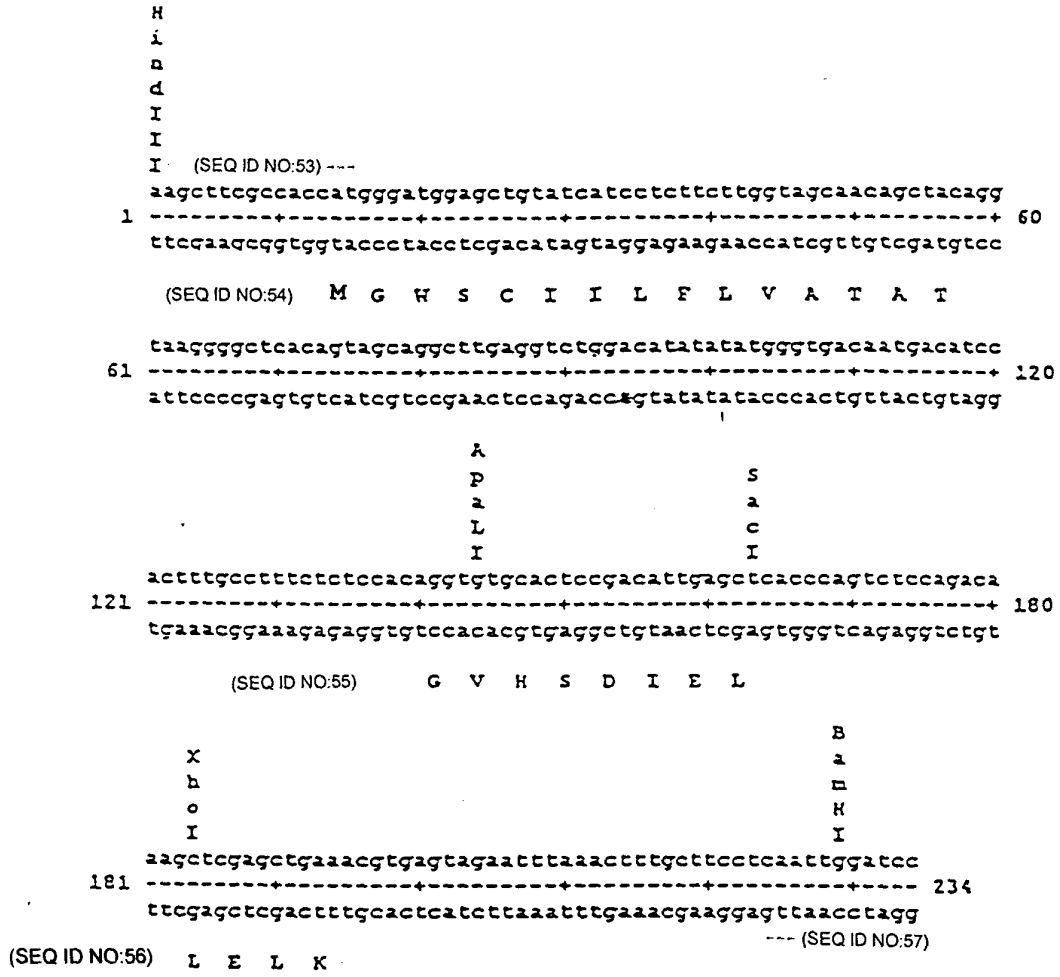


FIGURE 7

Fig.8.

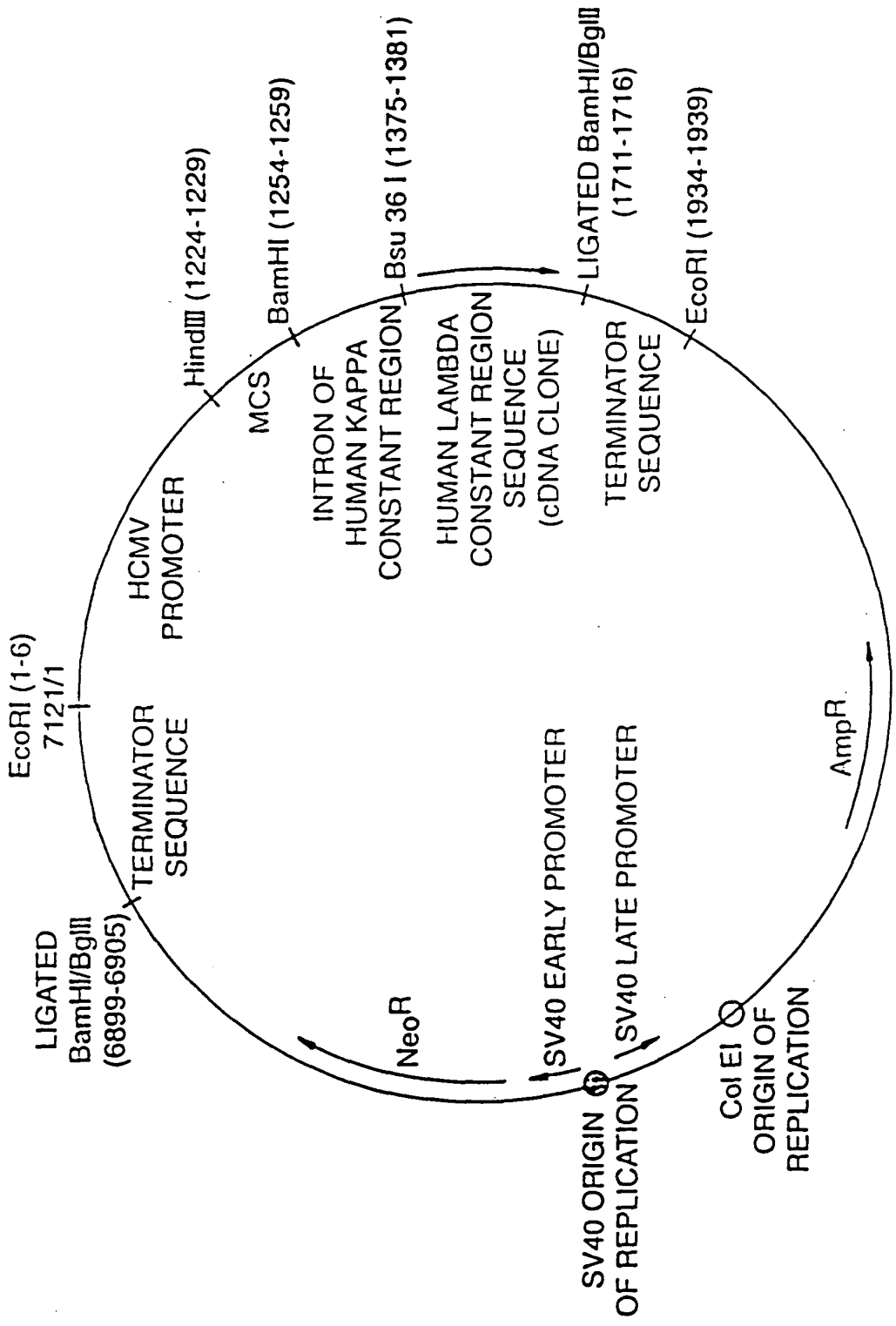

EcoRI (1-6)
7121/1
HCMV
PROMOTER
HindIII (1224-1229)
MCS
BamHI (1254-1259)
INTRON OF
HUMAN KAPPA
CONSTANT REGION
Bsu 36 I (1375-1381)
HUMAN LAMBDA
CONSTANT REGION
SEQUENCE
(cDNA CLONE)
LIGATED BamHI/BglII
(1711-1716)
TERMINATOR
SEQUENCE
EcoRI (1934-1939)
AmpR
Col EI
ORIGIN OF
REPLICATION
SV40 LATE PROMOTER
SV40 EARLY PROMOTER
SV40 ORIGIN
OF REPLICATION
NeoR
LIGATED
BamHI/BglII
(6899-6905)
TERMINATOR
SEQUENCE

Fig.9.

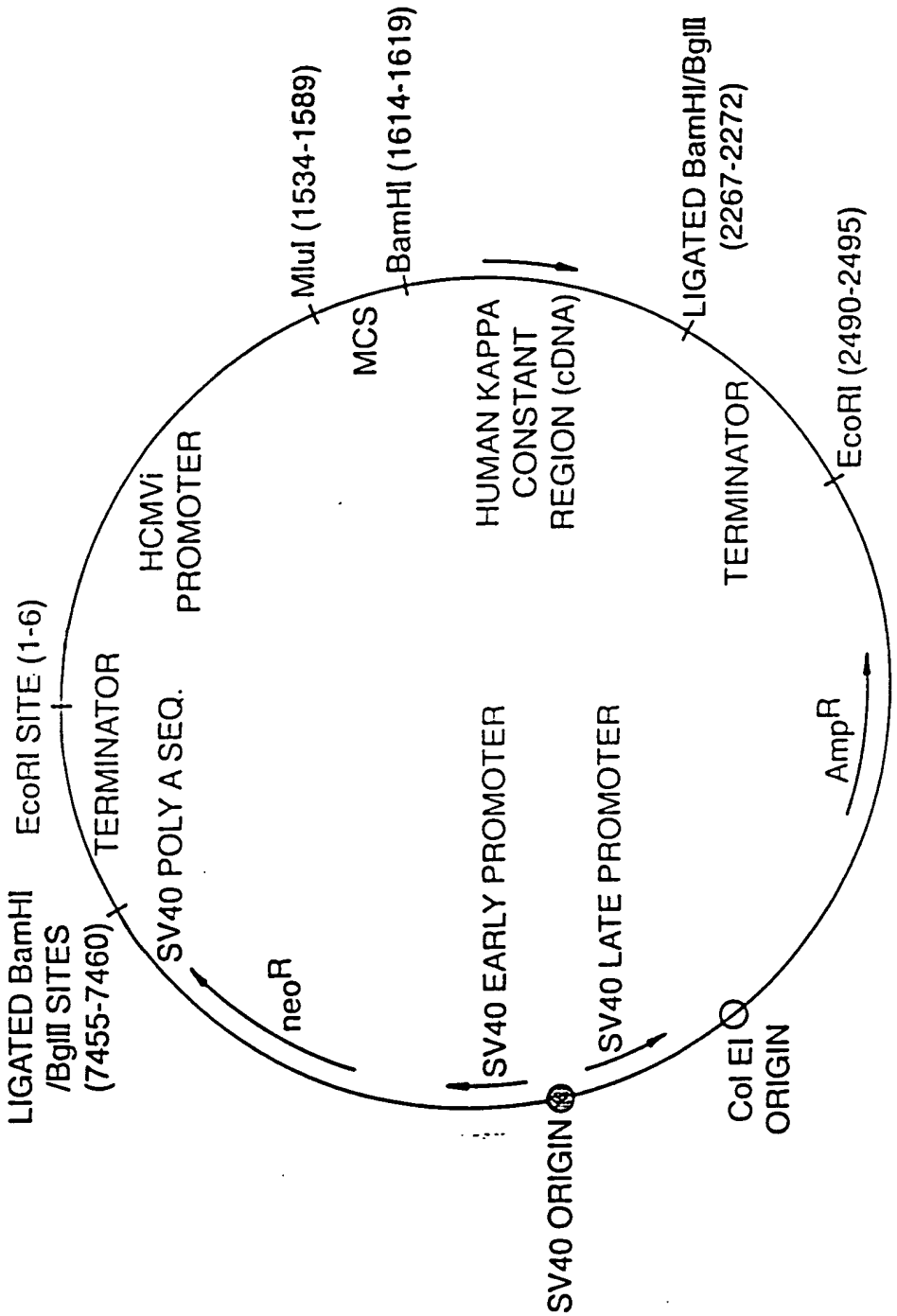

LIGATED BamHI /BglII SITES (7455-7460)
EcoRI SITE (1-6)
TERMINATOR
SV40 POLY A SEQ.
HCMVi PROMOTER
MluI (1534-1589)
BamHI (1614-1619)
MCS
HUMAN KAPPA CONSTANT REGION (cDNA)
LIGATED BamHI/BglII (2267-2272)
TERMINATOR
EcoRI (2490-2495)
AmpR
ColEI ORIGIN
SV40 ORIGIN
neoR
SV40 EARLY PROMOTER
SV40 LATE PROMOTER

Fig.10.

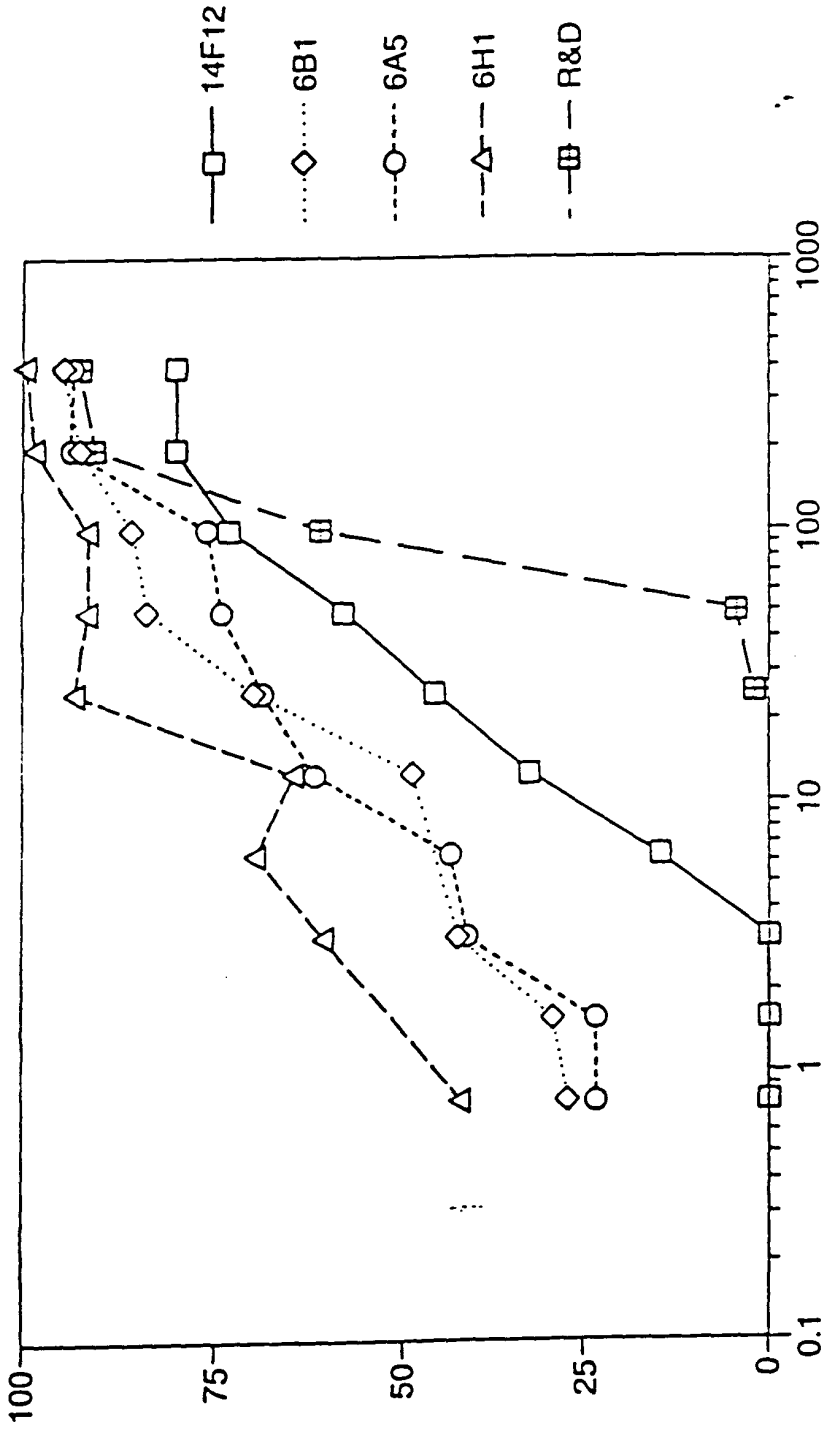


Fig.11.

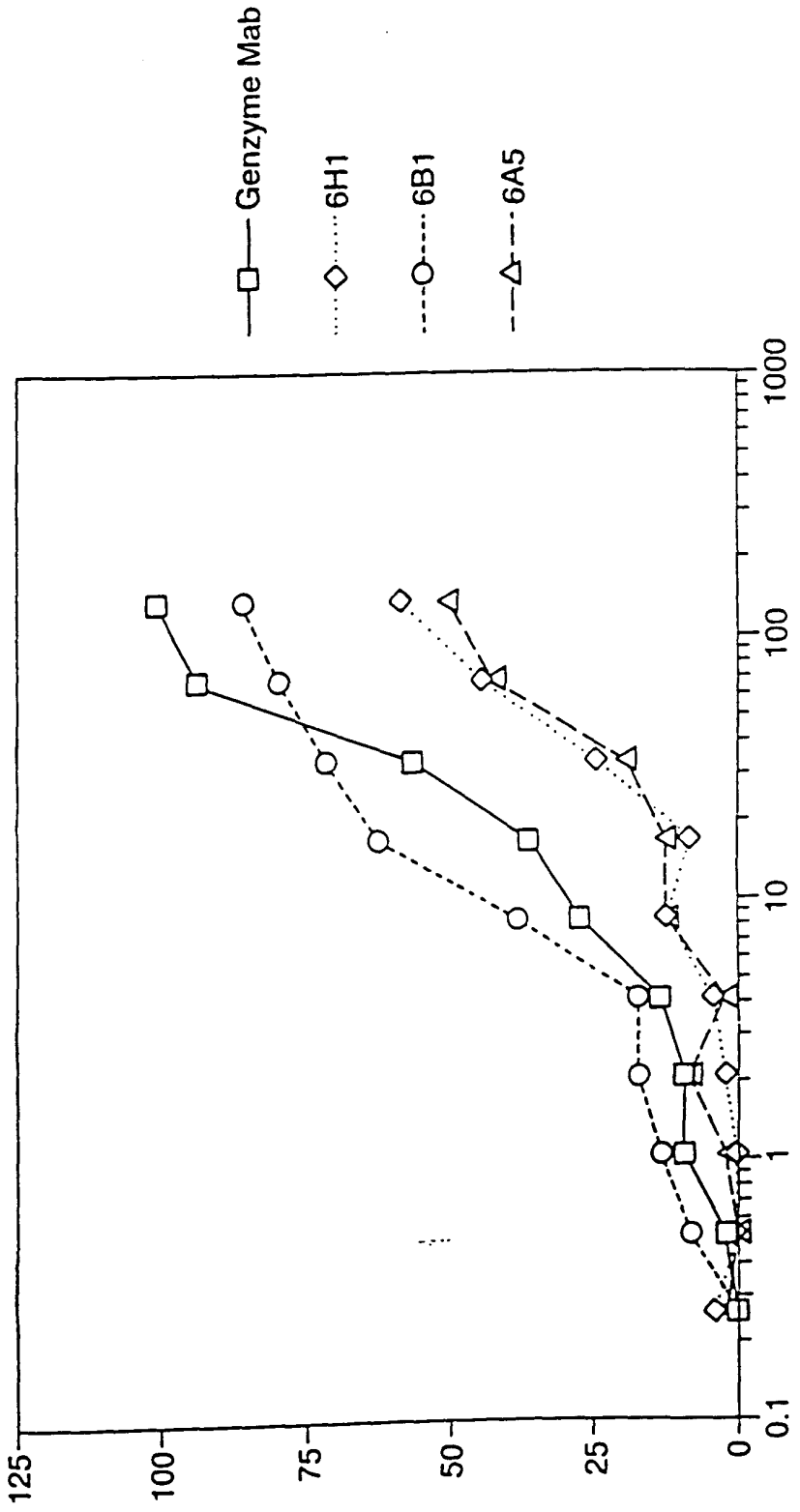


Fig.12.

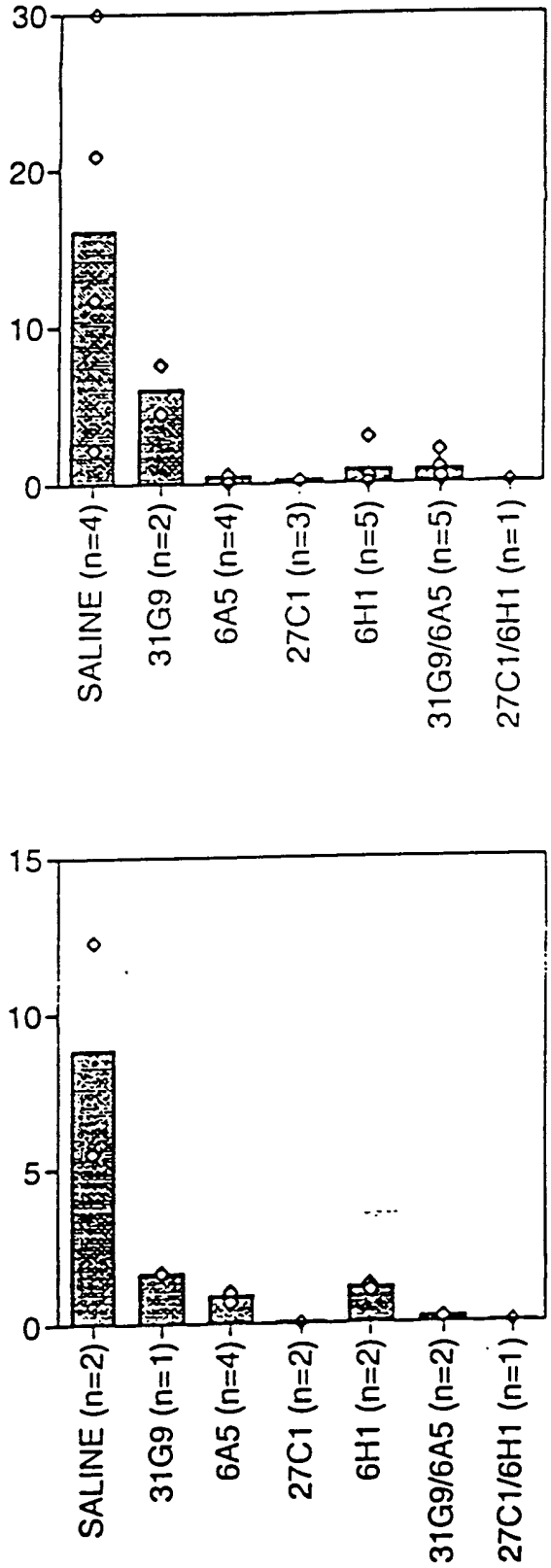

30
20
10
0
SALINE (n=4)
31G9 (n=2)
6A5 (n=4)
27C1 (n=3)
6H1 (n=5)
31G9/6A5 (n=5)
27C1/6H1 (n=1)
15
10
5
0
SALINE (n=2)
31G9 (n=1)
6A5 (n=4)
27C1 (n=2)
6H1 (n=2)
31G9/6A5 (n=2)
27C1/6H1 (n=1)

Fig.13(a).

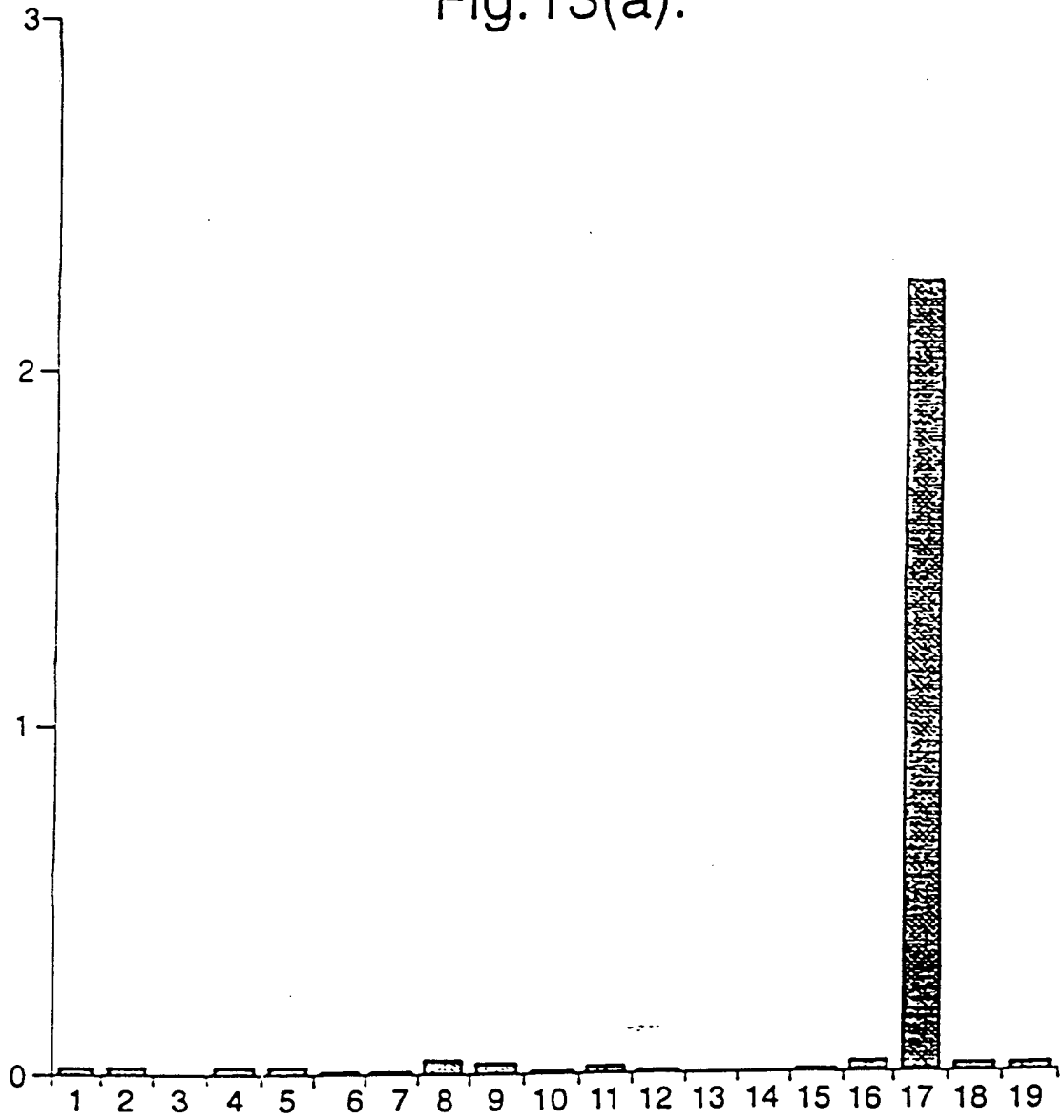


Fig.13(b).

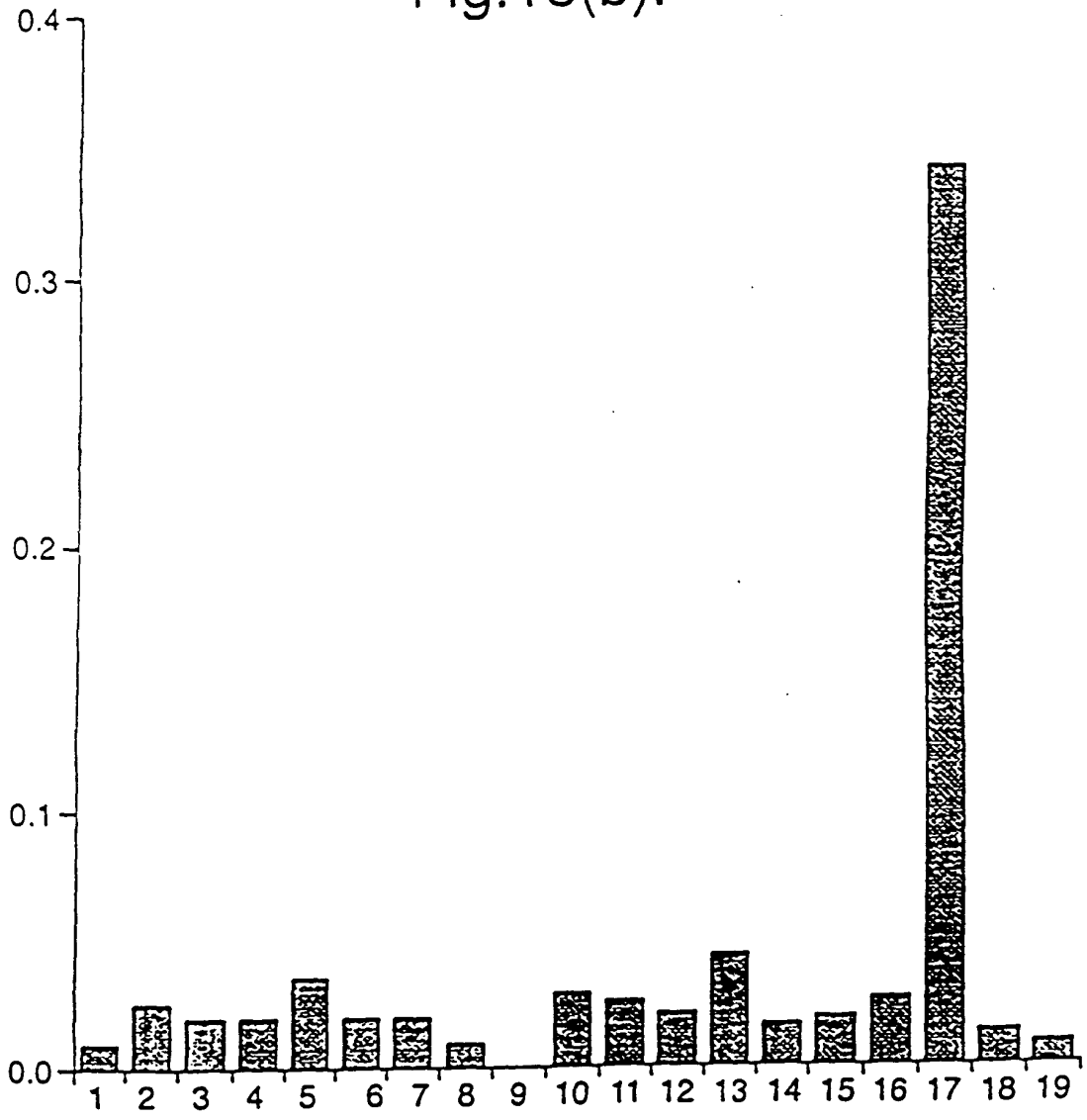


Figure 14

```
          10          20          30          40
GAA ATT GTG CTG ACT CAG TCT CCA TCC TCC CTG TCT GCA TCT GTA GGA
 E   I   V   L   T   Q   S   P   S   S   L   S   A   S   V   G>

50          60          70          80          90
GAC AGA GTC ACC ATC ACT TGC CGG GCA AGT CAG GGC ATT GGA GAT GAT
 D   R   V   T   I   T   C   R   A   S   Q   G   I   G   D   D>

  100         110         120         130         140
TTG GCC TGG TAT CAG CAG AAG CCA GGG AAA GCC CCT ATC CTC CTG ATC
 L   G   W   Y   Q   Q   K   P   G   K   A   P   I   L   L   I>

    150         160         170         180         190
TAT GGT ACA TCC ACT TTA CAA AGT GGG GTC CCG TCA AGG TTC AGC GGC
 Y   G   T   S   T   L   Q   S   G   V   P   S   R   F   S   G>

        200         210         220         230         240
AGT GGA TCT GGC ACA GAT TTC ACT CTC ACC ATC AAC AGC CTG CAG CCT
 S   G   S   G   T   D   F   T   L   T   I   N   S   L   Q   P>

          250         260         270         280
GAA GAT TTT GCA ACT TAT TAC TGT CTA CAA GAT TCC AAT TAC CCG CTC
 E   D   F   A   T   Y   Y   C   L   Q   D   S   N   Y   P   L>

290         300         310         320
ACT TTC GGC GGA GGG ACA CGA CTG GAG ATT AAA CGT (SEQ ID NO:58)
 T   F   G   G   G   T   R   L   E   I   K   R> (SEQ ID NO:59)
```

Fig.15.

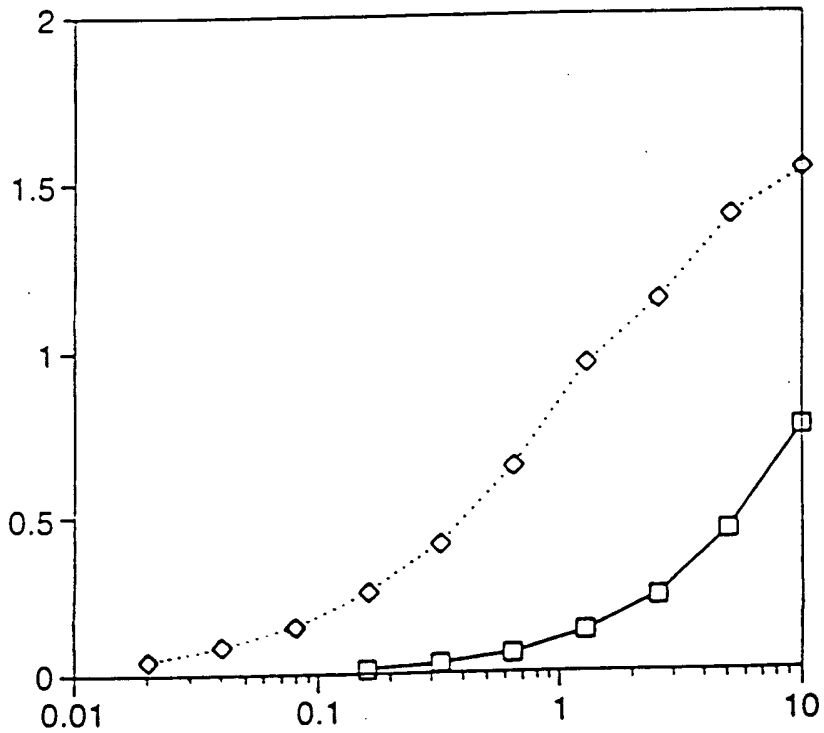


Fig.16.

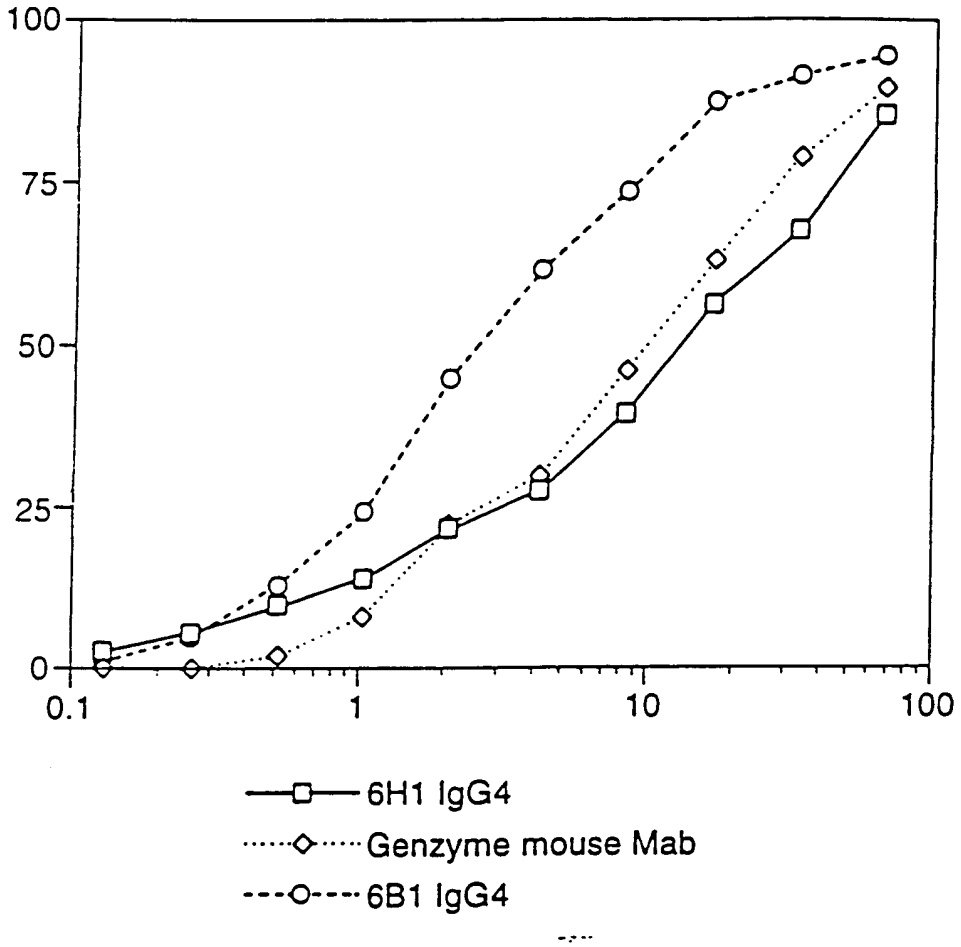


Fig.17.

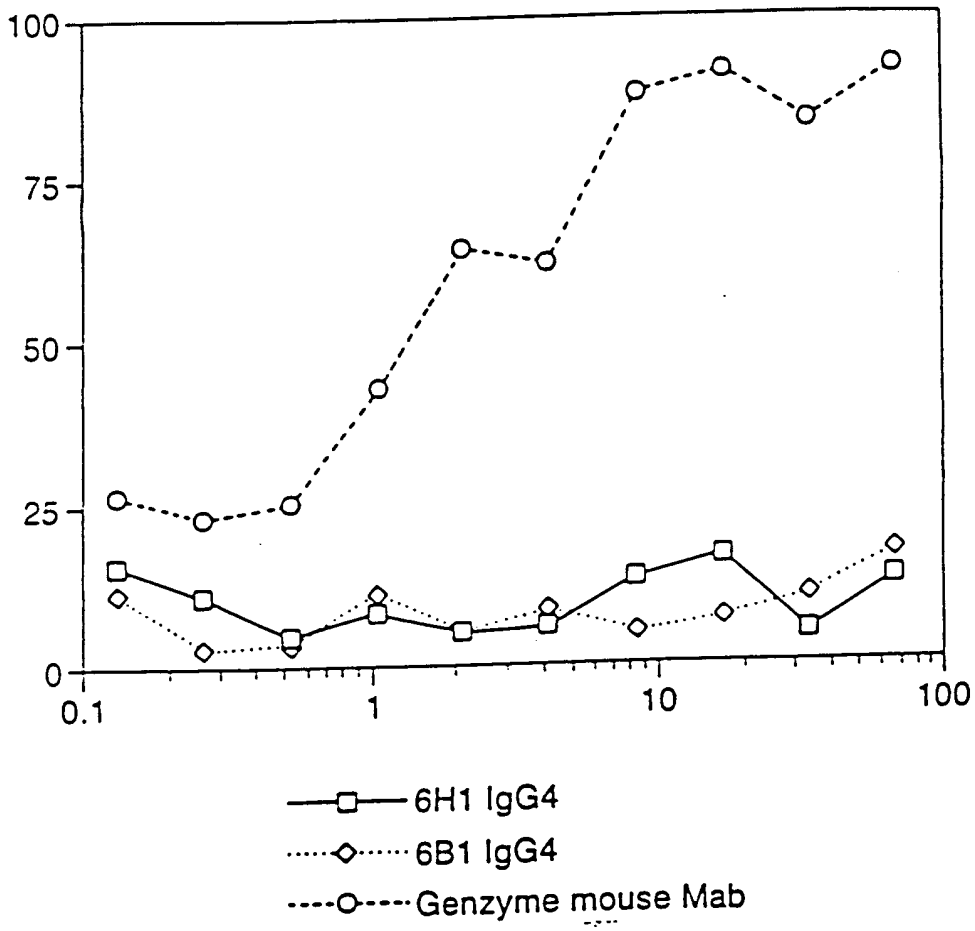


Fig.18.

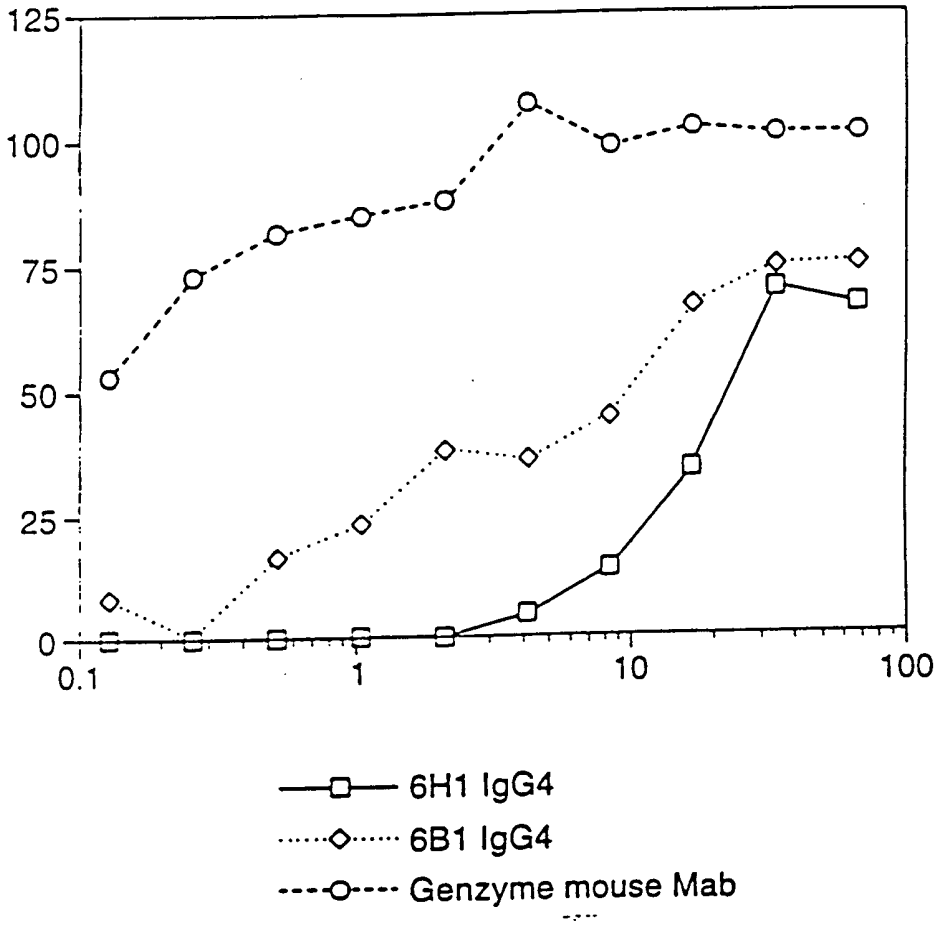

125
100
75
50
25
0
0.1
1
10
100
6H1 IgG4
6B1 IgG4
Genzyme mouse Mab

Figure 19

```
           10                  20                  30                  40
GAG GTG CAG CTG GTG GAG TCT GGG GGA GGC GTG GTC CAG CCT GGG AGG
 E   V   Q   L   V   E   S   G   G   G   V   V   Q   P   G   R>

50                  60                  70                  80                  90
TCC CTG AGA CTC TCC TGT GCA GCG TCT GGA TTC ACC TTC AGT AGC TAT
 S   L   R   L   S   C   A   A   S   G   F   T   F   S   S   Y>

  100                 110                 120                 130                 140
GGC ATG CAC TGG GTC CGC CAG GCT CCA GGC AAG GGG CTG GAG TGG GTG
 G   M   H   W   V   R   Q   A   P   G   K   G   L   E   W   V>

    150                 160                 170                 180                 190
GCA GTT ATA TGG TAT GAT GGA AGT AAT AAA TAC TAT GCA GAC TCC GTG
 A   V   I   W   Y   D   G   S   N   K   Y   Y   A   D   S   V>

        200                 210                 220                 230                 240
AAG GGC CGA TTC ACC ATC TCC AGA GAC AAT TCC AAG AAC ACG CTG TAT
 K   G   R   F   T   I   S   R   D   N   S   K   N   T   L   Y>

            250                 260                 270                 280
CTG CAA ATG GAC AGC CTG AGA GCC GAG GAC ACG GCC GTG TAT TAC TGT
 L   Q   M   D   S   L   R   A   E   D   T   A   V   Y   Y   C>

290                 300                 310                 320                 330
GGA AGA ACG CTG GAG TCT AGT TTG TGG GGC CAA GGC ACC CTG GTC ACC
 G   R   T   L   E   S   S   L   W   G   Q   G   T   L   V   T>

  340
GTC TCC TCA  (SEQ ID NO:60)
 V   S   S   (SEQ ID NO:61)
```

Figure 19 (ii)

```
                10                  20                  30                  40
TCG TCT GAG CTG ACT CAG GAC CCT GCT GTG TCT GTG GCC TTG GGA CAG
 S   S   E   L   T   Q   D   P   A   V   S   V   A   L   G   Q>

50                  60                  70                  80                  90
ACA GTC AGG ATC ACA TGC CAA GGA GAC AGC CTC AGA AGC TAT TAT GCA
 T   V   R   I   T   C   Q   G   D   S   L   R   S   Y   Y   A>

  100                 110                 120                 130                 140
AGC TGG TAC CAG CAG AAG CCA GGA CAG GCC CCT GTA CTT GTC ATC TAT
 S   W   Y   Q   Q   K   P   G   Q   A   P   V   L   V   I   Y>

    150                 160                 170                 180                 190
GGT AAA AAC AAC CGG CCC TCA GGG ATC CCA GAC CGA TTC TCT GGC TCC
 G   K   N   N   R   P   S   G   I   P   D   R   F   S   G   S>

        200                 210                 220                 230                 240
AGC TCA GGA AAC ACA GCT TCC TTG ACC ATC ACT GGG GCT CAG GCG GAA
 S   S   G   N   T   A   S   L   T   I   T   G   A   Q   A   E>

            250                 260                 270                 280
GAT GAG GCT GAC TAT TAC TGT AAC TCC CGG GAC AGC AGT AGT ACC CAT
 D   E   A   D   Y   Y   C   N   S   R   D   S   S   S   T   H>

290                 300                 310                 320                 330
CGA GGG GTG TTC GGC GGA GGG ACC AAG CTG ACC GTC CTA GGT (SEQ ID NO:62)
 R   G   V   F   G   G   G   T   K   L   T   V   L   G (SEQ ID NO:63)
```

Figure 19 (iii)

```
          10          20          30          40
TCG TCT GAG CTG ACT CAG GAC CCT GCT GTG TCT GTG GCC TTG GGA CAG
 S   S   E   L   T   Q   D   P   A   V   S   V   A   L   G   Q>

50          60          70          80          90
ACA GTC AGG ATC ACA TGC CAA GGA GAC AGC CTC AGA AGC TAT TAT GCA
 T   V   R   I   T   C   Q   G   D   S   L   R   S   Y   Y   A>

 100         110         120         130         140
AGC TGG TAC CAG CAG AAG CCA GGA CAG GCC CCT GTA CTT GTC ATC TAT
 S   W   Y   Q   Q   K   P   G   Q   A   P   V   L   V   I   Y>

    150         160         170         180         190
GGT AAA AAC AAC CGG CCC TCA GGG ATC CCA GAC CGA TTC GCT GGC TCC
 G   K   N   N   R   P   S   G   I   P   D   R   F   A   G   S>

        200         210         220         230         240
AAC TCA GGA AAC ACA GCT TCC TTG ACC ATC ACT GGG GCT CAG GCG GAG
 N   S   G   N   T   A   S   L   T   I   T   G   A   Q   A   E>

          250         260         270         280
GAT GAG GCT GAC TAT TAC TGT AGC TCC CGG GAC AGC AGT GGT AAC CAT
 D   E   A   D   Y   Y   C   S   S   R   D   S   S   G   N   H>

290         300         310         320
GTG GTT TTC GGC GGA GGG ACC AAG CTG ACC GTC CTA GGT
 V   V   F   G   G   G   T   K   L   T   V   L   G
```

(SEQ ID NO:64)
(SEQ ID NO:65)

Figure 19(iv)

```
          10          20          30          40
GAT GTT GTG ATG ACT CAG TCT CCA TCC TCC CTG TCT GCA TCT GTA GGA
 D   V   V   M   T   Q   S   P   S   S   L   S   A   S   V   G>

50          60          70          80          90
GAC AGA GTC ACC ATC ACT TGC CGG GCC AGT CAG GGC ATT AGC AAT TAT
 D   R   V   T   I   T   C   R   A   S   Q   G   I   S   N   Y>

  100         110         120         130         140
TTA GCC TGG TAT CAG CAA AAA CCA GGG AAA GCC CCT AAG CTC CTG ATC
 L   A   W   Y   Q   Q   K   P   G   K   A   P   K   L   L   I>

    150         160         170         180         190
TAT AAG GCA TCT ACT TTA GAA AGT GGG GTC CCA TCA AGG TTC AGT GGC
 Y   K   A   S   T   L   E   S   G   V   P   S   R   F   S   G>

       200         210         220         230         240
AGT GGA TCT GGG ACA GAA TTC ACT CTC ACA ATC AGC AGT CTG CAA CCT
 S   G   S   G   T   E   F   T   L   T   I   S   S   L   Q   P>

          250         260         270         280
GAA GAT TTT GCA ACT TAC TAC TGT CAA CAG AGT TAC AGT ACC CCT CGA
 E   D   F   A   T   Y   Y   C   Q   Q   S   Y   S   T   P   R>

290         300         310         320
ACG TTC GGC CAA GGG ACC AAA GTG GAT ATC AAA CGT  (SEQ ID NO:66)
 T   F   G   Q   G   T   K   V   D   I   K   R  (SEQ ID NO:67)
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Fig.20.

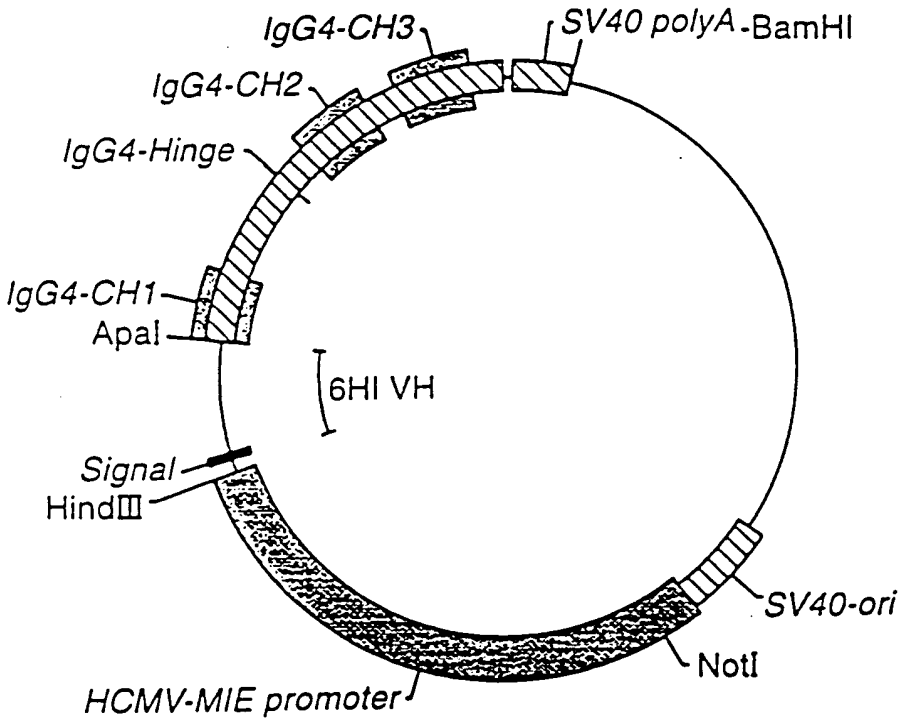

IgG4-CH3
SV40 polyA
BamHI
IgG4-CH2
IgG4-Hinge
IgG4-CH1
ApaI
6HI VH
Signal
HindIII
SV40-ori
NotI
HCMV-MIE promoter

Fig.21.

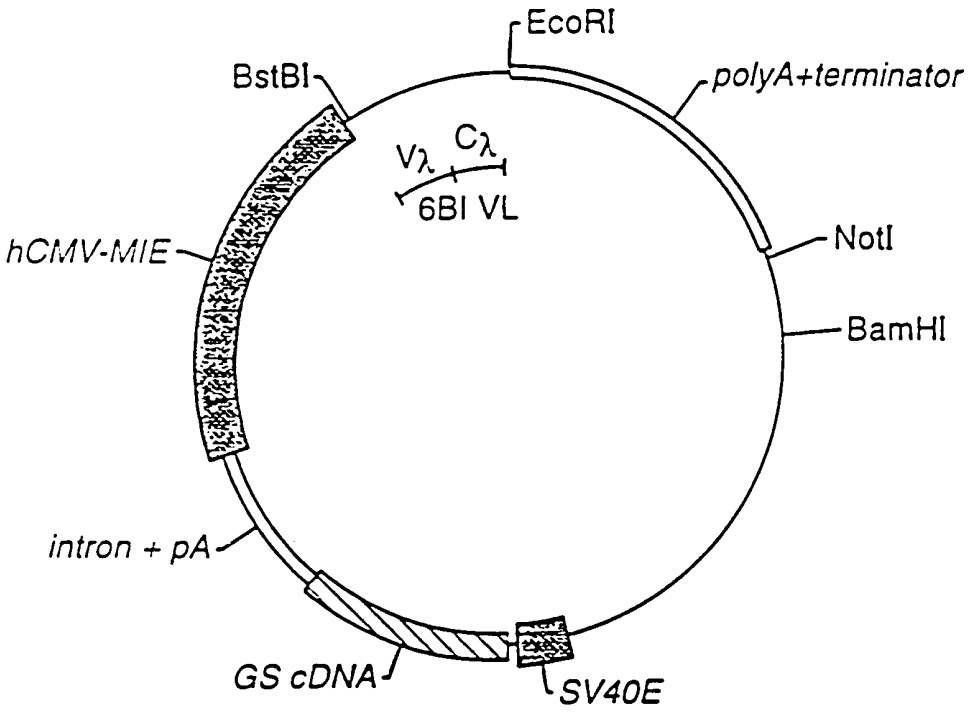

EcoRI
BstBI
polyA+terminator
Vλ Cλ
6BI VL
NotI
hCMV-MIE
BamHI
intron + pA
GS cDNA
SV40E

Fig.22.

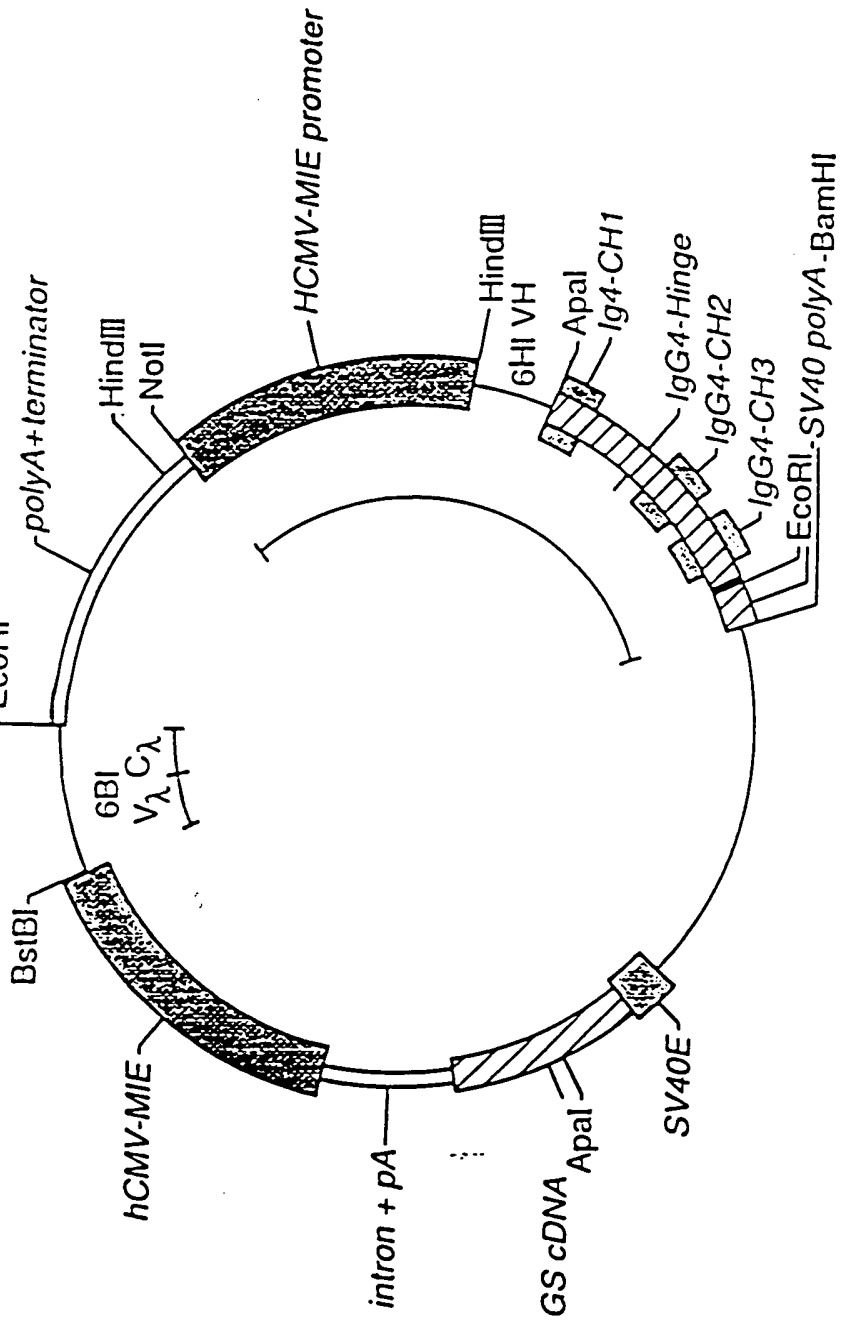
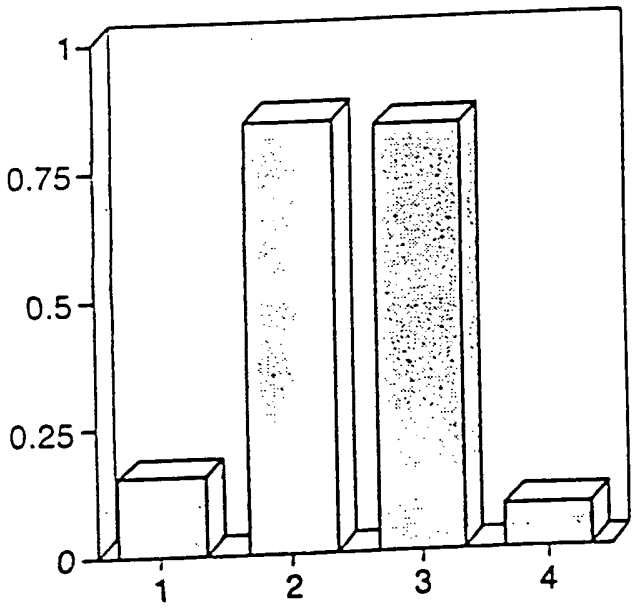
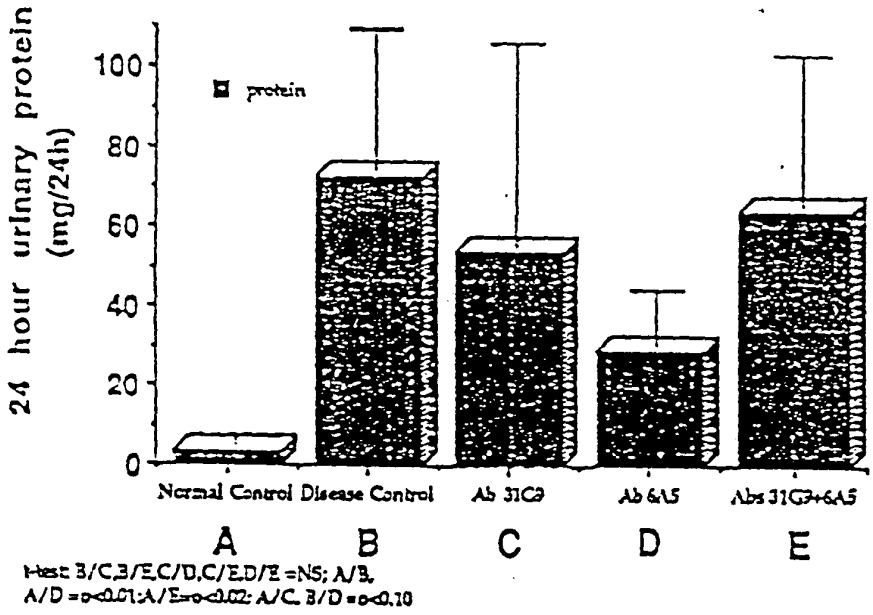

EcoRI
polyA+terminator
HindIII
NotI
HCMV-MIE promoter
HindIII
6HI VH
ApaI
Ig4-CH1
IgG4-Hinge
IgG4-CH2
IgG4-CH3
EcoRI-SV40 polyA-BamHI
6BI
Vλ Cλ
BstBI
hCMV-MIE
intron + pA
GS cDNA
ApaI
SV40E

Fig.23.





t-test: B/C,B/E,C/D,C/E,D/E =NS; A/B, A/D =p<0.01;A/E=p<0.02; A/C, B/D =p<0.10

FIGURE 24

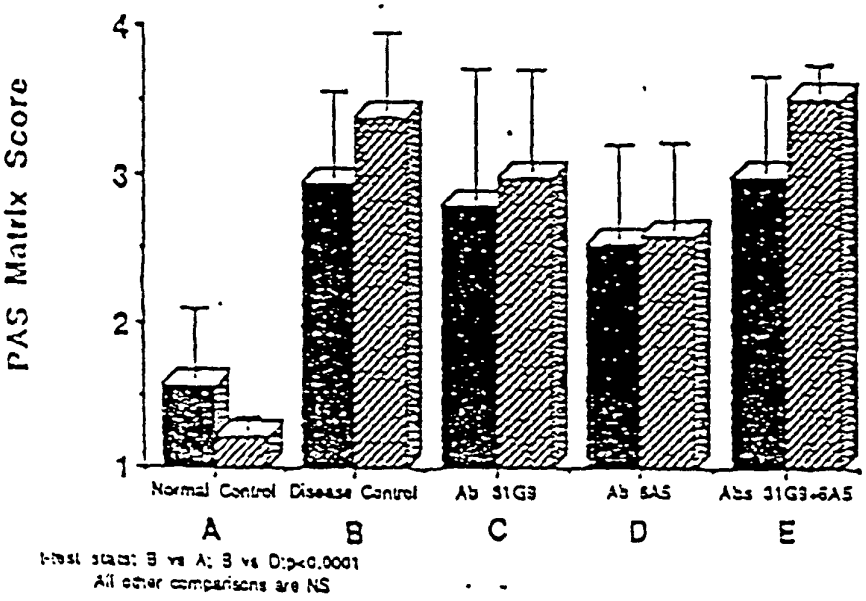

PAS Matrix Score
4
3
2
1
Normal Control
Disease Control
Ab 31G9
Ab 6A5
Abs 31G9+6A5
A
B
C
D
E
t-test stats: B vs A; B vs D:p<0.0001
All other comparisons are NS

FIGURE 25